

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 21, 2006, 04:16:59 ; Search time 194 Seconds  
(without alignments)  
322.880 Million cell updates/sec

Title: US-10-781-581-226

Perfect score: 725

Sequence: 1 AVTKPRYQMREIWSSTSTL.....HQLSHRLPMAENGRDGYL 137

Scoring table: BLOSUM62

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq.8: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003s: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*  
9: geneseqp2005s: \*  
10: geneseqp2006s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	725	100.0	137	8	ADR05215	Adt05215 Human ino
2	725	100.0	604	5	ABB09774	Abb09774 Amino aci
3	725	100.0	604	5	ABB09784	Abb09784 Amino aci
4	725	100.0	660	5	AAE16280	AAe16280 Human kin
5	725	100.0	683	5	ABU65211	ABu65211 Human NOV
6	725	100.0	683	9	ADN62073	ADn62073 Human nov
7	725	100.0	687	9	AE887638	AEb87638 Human ino
8	725	100.0	687	4	AA413393	AAa41393 Human pol
9	725	100.0	711	4	AA33607	AAa33607 Human pol
10	504	69.5	461	5	ABB09772	Abb09772 Amino aci
11	504	69.5	461	8	ADO44008	Ado44008 Amino aci
12	504	69.5	461	5	AE887636	AEb87636 Human ino
13	504	69.5	477	5	ABB09782	Abb09782 Amino aci
14	493	68.0	472	5	ABB09773	Abb09773 Amino aci
15	493	68.0	472	5	ABB09783	Abb09783 Amino aci
16	493	68.0	798	4	AAE04364	AAe04364 Human kin
17	493	68.0	946	9	AE887637	AEb87637 Human ino
18	482	66.5	1192	8	ADR40445	Adr40445 Mouse ino
19	464	64.0	1339	5	ABG65653	ABg65653 Human bre
20	403.5	55.7	382	4	ABBS8311	ABb58311 Drosophil
21	403.5	55.7	669	5	ABB09771	Abb09771 Amino aci
22	403.5	55.7	669	5	ABB09781	Abb09781 Amino aci
23	382.5	52.8	316	5	AAE26203	AAe26203 Maize ino

24	259.5	35.8	441	5	ABB09770	Abb09770 Amino aci
25	259.5	35.8	441	5	ABB09780	Abb09780 Amino aci
26	145	20.0	71	8	ABO56198	ABo56198 Human gen
27	83	11.4	1051	8	ADT66570	Adt66570 Rat Lut2p
28	81.5	11.2	325	7	ADU69714	AdJ69714 Human hea
29	80.5	11.1	349	8	ADN17522	Adn17522 Bacterial
30	79.5	11.0	248	3	AA645592	AAg45592 Arabidops
31	79.5	11.0	281	9	ADX84866	Adx84866 Inositol
32	79.5	11.0	286	9	ADX84903	Adx84903 Inositol
33	79.5	11.0	286	9	ADX84882	Adx84882 Inositol
34	79.5	11.0	293	9	ADX84864	Adx84864 Inositol
35	79.5	11.0	300	3	AA645591	AAg45591 Arabidops
36	79.5	11.0	300	9	ADX84881	Adx84881 Inositol
37	79.5	11.0	300	9	ADX84859	Adx84859 Inositol
38	79.5	11.0	300	9	ADX84880	Adx84880 Inositol
39	79.5	11.0	330	3	AA645590	AAg45590 Arabidops
40	78.5	10.8	1067	8	ADT66572	Adt66572 Murine lu
41	78	10.8	279	5	AAE26197	AAe26197 Soybean i
42	77	10.6	298	7	ADM25727	Adm25727 Hyperther
43	75.5	10.4	977	5	ABG97350	ABg97350 Human GGD
44	75	10.3	317	8	ADX88455	Adx88455 Plant ful
45	75	10.3	455	8	ADX73267	Adx73267 Plant ful

#### ALIGNMENTS

RESULT 1	ADR05215	standard; protein, 137 AA.
AD	ADR05215	
AC	ADR05215	
XX	21-OCT-2004	(first entry)
DT	Human inositol 1,4,5-triphosphate 3-kinase C (ITPKC) protein.	
XX		
DE		
XX		
KW	apoptosis; cytoskeletal; antiinflammatory; antiasthmatic; respiratory;	
KW	antipneumia; antiarthritic; gynaecological; cardiac; vasotropic;	
KW	antiproliferative; antiulcer; gastrointestinal; immunosuppressive;	
KW	neuroprotective; cancer; autoimmune; neurodegenerative; inflammatory;	
KW	asthma; chronic obstructive pulmonary disease; cystic fibrosis;	
KW	rheumatoid arthritis; acute respiratory distress syndrome; preclampsia;	
KW	myocardial ischemia; reperfusion injury; psoriasis; bronchiolitis;	
KW	Crohn's disease; ulcerative colitis; inflammatory bowel disease; human;	
KW	enzyme; inositol 1,4,5-triphosphate 3-kinase C; ITPKC.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004065959-A2.	
XX		
PD	05-AUG-2004.	
XX		
PF	23-JAN-2004; 2004WO-GB000271.	
XX		
PR	23-JAN-2003; 2003GB-00001566.	
XX		
PR	25-MAR-2003; 2003US-0457533P.	
XX		
PA	(EIRX-) EIRX THERAPEUTICS LTD.	
XX		
PI	Seery L, Hayes I, Murphy F;	
XX		
DR	WPI, 2004-S93556/57.	
XX		
DR	N-PSDB; ADR05216.	
XX		
PT	Identifying a modulator of apoptosis-associated polypeptide function,	
XX	useful for treating e.g., cancer, comprises incubating a sample	
PT	containing an apoptosis-associated polypeptide and a candidate agent to	
XX	permeic binding.	
XX		
PS	Claim 1; Page; 230pp; English.	
XX		
CC	The invention relates to a novel method for identifying an agent that	

CC modulates the function of an apoptosis-associated polypeptide,  
CC particularly a kinase or GPCR (G-protein-coupled receptor). The method  
CC comprises providing a sample containing an apoptosis-associated  
CC polypeptide and a candidate agent and incubating under conditions to  
CC permit binding of the candidate agent to the polypeptide, measuring the  
CC binding and comparing it with the binding of the polypeptide to a control  
CC agent known not to bind to the polypeptide. The method of the invention  
CC has cytostatic, antiinflammatory, antiaesthetic, respiratory,  
CC antineumatic, antiarthritic, gynaecological, cardiac, vasotropic,  
CC antidiabetic, antitumor, gastroenterical, immunosuppressive and  
CC neuroprotective applications. The method and molecules may be useful for  
CC treating a disease or condition characterised by abnormal apoptosis in  
CC mammalian tissue, particularly cancer, such as small cell lung cancer,  
CC cancer of the kidney, uterus, prostate, bladder, ovary, colon and breast,  
CC leukemias, sarcomas and myelomas. Furthermore, autoimmune,  
CC neurodegenerative and inflammatory conditions may be treated, including  
CC asthma, chronic obstructive pulmonary disease, cystic fibrosis,  
CC rheumatoid arthritis, acute respiratory distress syndrome, preclampsia,  
CC myocardial ischaemia, reperfusion injury, psoriasis, bronchiolitis,  
CC Crohn's disease, ulcerative colitis and inflammatory bowel disease. The  
CC current sequence is that of a human apoptosis-associated protein of the  
CC invention which was used during siRNA (small interfering RNA)-mediated  
CC gene silencing.  
CC  
CC  
SQ Sequence 137 AA;

Query Match 100.0%; Score 725; DB 8; Length 137;  
Best Local Similarity 100.0%; Pred. No. 6,3e-75;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTKPRMOMREMTSSTSLGFRLEGKKADGTCNTNFKTKQALBQYTKVLEDFVDDGHV 60  
DB 1 AVTKPRMOMREMTSSTSLGFRLEGKKADGTCNTNFKTKQALBQYTKVLEDFVDDGHV 60  
QY 61 ILQKYVACLBEELREALEISPPFKTHEVVGSSLLFVHDHTGLAKYMWIDFGKTVALPDHQT 120  
DB 61 ILQKYVACLBEELREALEISPPFKTHEVVGSSLLFVHDHTGLAKYMWIDFGKTVALPDHQT 120  
QY 121 LSHRLPWAEGNREDGYL 137  
DB 121 LSHRLPWAEGNREDGYL 137

## RESULT 2

ABB09774 ID ABB09774 standard; protein; 604 AA.

XX ABB09774;

DT 22-JUL-2002 (first entry)

DE Amino acid sequence of human inositol-1,4,5-triphosphate 3 kinase-C.  
XX  
XX IP3 kinase; inositol-1,4,5-triphosphate kinase; enzyme; oxidative stress;  
XX endoplasmic reticulum stress; neurodegeneration; retina; free radical;  
XX chronic infection; arthritis; cancer; cystic fibrosis;  
XX Alzheimer's disease; Huntington's disease; pigmentary retinopathy;  
XX DIP3K1; DIP3K2.

XX Homo sapiens.

XX OS

XX FR2813612-A1.

XX PD 08-MAR-2002.

XX PF 07-SEP-2000; 2000FR-00011397.

XX PR 07-SEP-2000; 2000FR-00011397.

XX PA (CNRS ) CNRS CENT NAT RECH SCI.

XX PI Tricoire H, Monnier V, Pret AM, Cabet DE, Briesard J, Vandurka P,  
XX Girardot F;

XX WPI: 2002-260343/31.  
DR N-PSDB; ABL56446.  
XX  
XX New proteins with inositol-triphosphate kinase activity, useful e.g. for  
PT treating oxidative stress and neurodegeneration.  
XX  
XX Claim 4; Fig 5; 69pp; French.

XX The present sequence represents inositol-1,4,5-triphosphate 3 (IP3)  
CC kinase-C protein. The specification also describes prosophila IP3 kinase  
CC proteins, designated DIP3K1 and DIP3K2. This protein has IP3 (inositol-  
CC 1,4,5-triphosphate) kinase activity. The specification describes the use  
CC of IP3 kinase proteins to prepare compositions for treating diseases  
CC associated with oxidative stress, stress of the endoplasmic reticulum or  
CC neurodegeneration, particularly of the retina. Overexpression of IP3  
CC kinase protects cells against the damaging effects of free radicals  
CC without altering free radical homeostasis within the cell. The IP3  
CC proteins are used for treating disorders associated with oxidative  
CC stress, stress on the endoplasmic reticulum and neurodegeneration,  
CC particularly chronic infection (such as arthritis and some forms of  
CC cancer); cystic fibrosis; Alzheimer's and Huntington's diseases, and  
CC pigmentary retinopathy. Transgenic animals that lack the gene for IP3  
CC kinase proteins are used to identify phenotypic alterations associated  
CC with loss of this gene  
CC  
CC  
SQ Sequence 604 AA;

Query Match 100.0%; Score 725; DB 5; Length 604;  
Best Local Similarity 100.0%; Pred. No. 4,9e-74;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTKPRMOMREMTSSTSLGFRLEGKKADGTCNTNFKTKQALBQYTKVLEDFVDDGHV 60  
DB 452 AVTKPRMOMREMTSSTSLGFRLEGKKADGTCNTNFKTKQALBQYTKVLEDFVDDGHV 511  
QY 61 ILQKYVACLBEELREALEISPPFKTHEVVGSSLLFVHDHTGLAKYMWIDFGKTVALPDHQT 120  
DB 512 ILQKYVACLBEELREALEISPPFKTHEVVGSSLLFVHDHTGLAKYMWIDFGKTVALPDHQT 571  
QY 121 LSHRLPWAEGNREDGYL 137  
DB 572 LSHRLPWAEGNREDGYL 588

## RESULT 3

ABB09784 ID ABB09784 standard; protein; 604 AA.

XX ABB09784;

DT 22-JUL-2002 (first entry)

DE Amino acid sequence of human inositol-1,4,5-triphosphate 3 kinase-C.  
XX  
XX IP3 kinase; inositol-1,4,5-triphosphate kinase; enzyme; oxidative stress;  
XX endoplasmic reticulum stress; neurodegeneration; retina; free radical;  
XX chronic infection; arthritis; cancer; cystic fibrosis;  
XX Alzheimer's disease; Huntington's disease; pigmentary retinopathy;  
XX DIP3K1; DIP3K2.

XX Homo sapiens.

XX OS

XX WO200220742-A1.

XX PD 14-MAR-2002.

XX PF 31-AUG-2001; 2001WO-FR002708.

XX PR 07-SEP-2000; 2000FR-00011397.

XX PA (CNRS ) CENT NAT RECH SCI.



RESULT 5  
ABU65211  
ID ABU65211 standard; protein; 683 AA.  
XX  
XX ABU65211;  
AC  
XX  
XX 20-MAY-2003 (first entry)  
DT  
XX  
XX Human NOV123a protein.  
DE  
XX  
XX NOXV; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;  
KM hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;  
XX human.  
XX  
XX Homo sapiens.  
PN WO200272757-A2.  
PD 19-SEP-2002.  
PF 08-MAR-2002; 2002MO-US006908.  
XX  
XX 08-MAR-2001; 2001US-0274101P.  
PR 08-MAR-2001; 2001US-0274194P.  
PR 08-MAR-2001; 2001US-0274281P.  
PR 08-MAR-2001; 2001US-0274322P.  
PR 09-MAR-2001; 2001US-0274849P.  
PR 12-MAR-2001; 2001US-0275235P.  
PR 13-MAR-2001; 2001US-0275578P.  
PR 13-MAR-2001; 2001US-0275579P.  
PR 13-MAR-2001; 2001US-0275601P.  
PR 14-MAR-2001; 2001US-0276000P.  
PR 15-MAR-2001; 2001US-0276776P.  
PR 19-MAR-2001; 2001US-0276999P.  
PR 20-MAR-2001; 2001US-0277233P.  
PR 20-MAR-2001; 2001US-0277321P.  
PR 21-MAR-2001; 2001US-0277321P.  
PR 21-MAR-2001; 2001US-0277791P.  
PR 22-MAR-2001; 2001US-0278833P.  
PR 23-MAR-2001; 2001US-0278152P.  
PR 26-MAR-2001; 2001US-0278894P.  
PR 27-MAR-2001; 2001US-0278999P.  
PR 27-MAR-2001; 2001US-0279036P.  
PR 28-MAR-2001; 2001US-0279344P.  
PR 30-MAR-2001; 2001US-0277338P.  
PR 30-MAR-2001; 2001US-0279995P.  
PR 30-MAR-2001; 2001US-0280233P.  
PR 02-APR-2001; 2001US-0280802P.  
PR 02-APR-2001; 2001US-0280822P.  
PR 02-APR-2001; 2001US-0280900P.  
PR 04-APR-2001; 2001US-0281194P.  
PR 13-APR-2001; 2001US-0283675P.  
PR 30-APR-2001; 2001US-0287424P.  
PR 03-MAY-2001; 2001US-0288066P.  
PR 03-MAY-2001; 2001US-0288342P.  
PR 03-MAY-2001; 2001US-0288528P.  
PR 15-MAY-2001; 2001US-0291190P.  
PR 16-MAY-2001; 2001US-0291099P.  
PR 16-MAY-2001; 2001US-0291240P.  
PR 30-MAY-2001; 2001US-0294485P.  
PR 31-MAY-2001; 2001US-0294899P.  
PR 31-MAY-2001; 2001US-0294899P.  
PR 18-JUN-2001; 2001US-0299027P.  
PR 19-JUN-2001; 2001US-0299030P.  
PR 19-JUN-2001; 2001US-0299310P.  
PR 10-JUL-2001; 2001US-0304354P.  
PR 31-JUL-2001; 2001US-0309198P.  
PR 16-AUG-2001; 2001US-0312903P.  
PR 10-SEP-2001; 2001US-0318462P.  
PR 12-SEP-2001; 2001US-0318770P.  
PR 27-SEP-2001; 2001US-0325430P.

PR 27-SEP-2001; 2001US-0325681P.  
PR 18-OCT-2001; 2001US-0330380P.  
PR 31-OCT-2001; 2001US-0335301P.  
PR 14-NOV-2001; 2001US-0332172P.  
PR 14-NOV-2001; 2001US-0332271P.  
PR 14-NOV-2001; 2001US-0332272P.  
PR 14-NOV-2001; 2001US-0333184P.  
PR 14-NOV-2001; 2001US-0333722P.  
PR 21-NOV-2001; 2001US-0332094P.  
PR 03-DEC-2001; 2001US-0337426P.  
PR 03-DEC-2001; 2001US-0338092P.  
PR 04-DEC-2001; 2001US-0337185P.  
PR 03-JAN-2002; 2002US-0345705P.  
PR 07-MAR-2002; 2002US-00092900.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CE, Li L,  
PI Zehrsen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;  
PI Patturajan M, Gangoli E, Vernet CM, Guo X, Tchernev V;  
PI Fernandes ER, Caeman SJ, Malyanar UM, Gerlach V, Liu Y, Anderson D;  
PI Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsdbrook JB;  
PI Lepley DW, Rieger DK;  
XX  
XX WPI: 2002-72332/78.  
DR N-PSDB; ABX97178.  
XX  
XX NOXV polypeptides and polynucleotides, useful for preventing or treating  
PT a disorder associated with aberrant NOXV expression or activity e.g.,  
PT cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial  
PT asthma.  
XX  
XX Claim 1; Page 461; 1103pp; English.  
PS  
XX  
XX This invention describes novel human NOXV polypeptides which have  
CC cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive  
CC activity. Pharmaceutical compositions comprising the NOXV proteins or  
CC nucleic acid molecules or NOXV antibodies are useful for preventing or  
CC treating a disorder associated with aberrant NOXV expression or activity  
CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial  
CC asthma. The products of the invention can be used for gene therapy or in  
CC a vaccine. ABU65041-ABU65218 represent the NOXV polypeptides encoded by  
CC ABX97008-ABX97185  
XX  
XX Sequence 683 AA;  
SQ  
Query Match 100.0%; Score 725; DB 5; Length 683;  
Best Local Similarity 100.0%; Pred. No. 5; 8e-74;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVTKPRVQWREMTSSSTTGFRTGKADGTCNTNPKTKQALEQVTKVLEDFVDDGHV 60  
DB 531 AVTKPRVQWREMTSSSTTGFRTGKADGTCNTNPKTKQALEQVTKVLEDFVDDGHV 590  
QY 61 ILQKYVACLEBELREALTSPFKEVHVGSSILFEVHDTGLAKYMTDFGKTVALPDHQT 120  
DB 531 ILQKYVACLEBELREALTSPFKEVHVGSSILFEVHDTGLAKYMTDFGKTVALPDHQT 650  
QY 121 LSHRLPMAEGNREDGYL 137  
DB 651 LSHRLPMAEGNREDGYL 667  
RESULT 6  
ADN62073  
ID ADN62073 standard; protein; 683 AA.  
XX  
XX ADN62073;  
AC  
XX  
XX 01-JUL-2004 (first entry)  
DT  
XX  
XX Human novel protein NOV123a.  
DE  
XX

KW Human; NOV; diabetes; obesity; infectious disease; anorexia;  
 cancer-associated cachexia; cancer; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; immune disorder;  
 KW haematopoietic disorder; dyslipidaemia; chronic disease.  
 OS Homo sapiens.  
 PN US2004043382-A1.  
 XX  
 XX  
 PD 04-MAR-2004.  
 XX  
 PF 07-MAR-2002; 2002US-00092900.  
 XX  
 PF 08-MAR-2001; 2001US-0274191P.  
 PR 08-MAR-2001; 2001US-0274194P.  
 PR 08-MAR-2001; 2001US-0274281P.  
 PR 08-MAR-2001; 2001US-0274322P.  
 PR 09-MAR-2001; 2001US-0274849P.  
 PR 12-MAR-2001; 2001US-0275235P.  
 PR 13-MAR-2001; 2001US-0275578P.  
 PR 13-MAR-2001; 2001US-0275579P.  
 PR 13-MAR-2001; 2001US-0275601P.  
 PR 14-MAR-2001; 2001US-027600P.  
 PR 16-MAR-2001; 2001US-0276776P.  
 PR 19-MAR-2001; 2001US-0276994P.  
 PR 20-MAR-2001; 2001US-0277239P.  
 PR 20-MAR-2001; 2001US-0277321P.  
 PR 20-MAR-2001; 2001US-0277327P.  
 PR 20-MAR-2001; 2001US-0277388P.  
 PR 21-MAR-2001; 2001US-0277791P.  
 PR 22-MAR-2001; 2001US-0278152P.  
 PR 23-MAR-2001; 2001US-0278152P.  
 PR 26-MAR-2001; 2001US-0278994P.  
 PR 27-MAR-2001; 2001US-0278999P.  
 PR 27-MAR-2001; 2001US-0279036P.  
 PR 28-MAR-2001; 2001US-0279344P.  
 PR 30-MAR-2001; 2001US-0279959P.  
 PR 30-MAR-2001; 2001US-0280233P.  
 PR 02-APR-2001; 2001US-0280802P.  
 PR 02-APR-2001; 2001US-0280823P.  
 PR 02-APR-2001; 2001US-0280900P.  
 PR 04-APR-2001; 2001US-0281444P.  
 PR 13-APR-2001; 2001US-0283675P.  
 PR 30-APR-2001; 2001US-0287424P.  
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 PR 03-MAY-2001; 2001US-0288342P.  
 PR 03-MAY-2001; 2001US-0288528P.  
 PR 15-MAY-2001; 2001US-0291190P.  
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 PR 30-MAY-2001; 2001US-0294485P.  
 PR 31-MAY-2001; 2001US-0294889P.  
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 PR 18-JUN-2001; 2001US-0299027P.  
 PR 19-JUN-2001; 2001US-0299303P.  
 PR 19-JUN-2001; 2001US-0299310P.  
 PR 10-JUL-2001; 2001US-0304354P.  
 PR 31-JUL-2001; 2001US-0309198P.  
 PR 16-AUG-2001; 2001US-0312903P.  
 PR 10-SEP-2001; 2001US-0318462P.  
 PR 12-SEP-2001; 2001US-0318770P.  
 PR 27-SEP-2001; 2001US-0325430P.  
 PR 27-SEP-2001; 2001US-0325681P.  
 PR 18-OCT-2001; 2001US-0330380P.  
 PR 31-OCT-2001; 2001US-0335301P.  
 PR 14-NOV-2001; 2001US-0332172P.  
 PR 14-NOV-2001; 2001US-0332271P.  
 PR 14-NOV-2001; 2001US-0332272P.  
 PR 14-NOV-2001; 2001US-0333184P.  
 PR 21-NOV-2001; 2001US-0333272P.  
 PR 03-DEC-2001; 2001US-0332099P.  
 PR 03-DEC-2001; 2001US-0337428P.  
 PR 03-DEC-2001; 2001US-0338092P.

PR 04-DEC-2001; 2001US-0337185P.  
 PR 03-JAN-2002; 2002US-0345705P.  
 XX  
 PA (PADI/) PADIGARU M.  
 PA (SPYT/) SPYTEK K A.  
 PA (SHEN/) SHENOY S G.  
 PA (TAUP/) TAUPIER R J.  
 PA (PEN/) PENNA C E A.  
 PA (LITL/) LI L.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (GUSE/) GUSEV V Y.  
 PA (JIMW/) JI W.  
 PA (GORM/) GORMAN L.  
 PA (MILL/) MILLER C E.  
 PA (KEKU/) KEKUDA R.  
 PA (PAT/) PATTURAJAN M.  
 PA (GANG/) GANGOLLI E A.  
 PA (VERN/) VERNET C A M.  
 PA (GUOX/) GUO X S.  
 PA (TCHE/) TCHERNEV V T.  
 PA (FERN/) FERNANDES E R.  
 PA (CASM/) CASMAN S J.  
 PA (MALY/) MALYANKAR U M.  
 PA (GERL/) GERLACH V.  
 PA (LITV/) LITV Y.  
 PA (ANDE/) ANDERSON D W.  
 PA (SPAD/) SPADERNA S K.  
 PA (CAT/) CATTERTON E.  
 PA (LEIT/) LEITTE M W.  
 PA (ZHON/) ZHONG H.  
 PA (ALSO/) ALSOBOOK J P.  
 PA (LEPL/) LEPLLEY D M.  
 PA (RIEG/) RIEGER D K.  
 PA (BURG/) BURGESS C E.  
 XX  
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 PI Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CE, Li L;  
 PI Zethusen BD, Gusev VY, Ji W, Gorman L, Miller CE, Kekuda R;  
 PI Patturajan M, Gangolli EA, Vernet CM, Guo XS, Tchernev VT;  
 PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y;  
 PI Anderson DW, Spaderna SK, Catterton E, Leite MW, Zhong H;  
 PI Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;  
 PI  
 DR WPI; 2004-225693/21.  
 DR N-PSDB; ADN62072.  
 XX  
 XX  
 PT New NOVX polypeptides and nucleic acid molecules useful for diagnosing,  
 PT preventing or treating NOVX-associated disorders, e.g. cancer, diabetes,  
 PT infection or obesity, and in chromosome mapping, tissue typing or  
 PT pharmacogenomics.  
 XX  
 PS Claim 1; SEQ ID NO 342; 786pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide (designated NOVX, or  
 CC NOV1-NOV127) comprising a sequence selected from 178 fully defined amino  
 CC acid sequences (and their mature forms, variants and fragments). Also  
 CC included are an isolated nucleic acid molecule encoding NOVX, a vector  
 CC comprising the nucleic acid, a cell comprising the vector, methods for  
 CC determining the presence or amount of the polypeptide or the nucleic acid  
 CC molecule in a sample, methods for determining the presence of or  
 CC predisposition to a disease associated with altered levels of expression  
 CC of the above polypeptide or nucleic acid molecule in a first mammalian  
 CC subject, a method for identifying an agent that binds to the above  
 CC polypeptide, a method for identifying a potential therapeutic agent for  
 CC use in the treatment of a pathology that is related to aberrant  
 CC expression or physiological interactions of the polypeptide, a method of  
 CC screening for a modulator of activity or of latency or predisposition to  
 CC a pathology associated with the polypeptide and a method for modulating  
 CC the activity of the polypeptide cited above. The composition and methods  
 CC are useful for diagnosing, preventing or treating diseases such as  
 CC diabetes, obesity, infectious diseases, anorexia, cancer-associated  
 CC cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or  
 CC Parkinson's disease, immune disorders, haematopoietic disorders, or  
 CC dyslipidaemias, and other chronic diseases. These may also be used in

CC chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. The polypeptides are also useful as vaccines. The  
CC present sequence represents a NOVX protein of the invention.

XX Sequence 683 AA;

Query Match 100.0%; Score 725; DB 8; Length 683;

Best Local Similarity 100.0%; Pred. No. 5.8e-74;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTKRYMQWRETMSTSTLGFRLEGIKKADGTCNTNFKKTOALEQYTKVLEDFVDDHV 60

DB 531 AVTKRYMQWRETMSTSTLGFRLEGIKKADGTCNTNFKKTOALEQYTKVLEDFVDDHV 590

QY 61 ILQKYVACLEBELRALISPEFKTHEVVGSSLLFVHDHTGLAKYWMIDFGKTVALPDHQT 120

DB 591 ILQKYVACLEBELRALISPEFKTHEVVGSSLLFVHDHTGLAKYWMIDFGKTVALPDHQT 650

QY 121 LSHRLPWAEGNREDGYL 137

DB 651 LSHRLPWAEGNREDGYL 667

RESULT 7

ID AEB87638 standard; protein; 683 AA.

AC AEB87638;

DT 20-OCT-2005 (first entry)

XX Human inositol-trisphosphate 3-kinase C (ITPKC).

XX Inositol-trisphosphate 3-kinase C; ITPKC;

KM insulin-like growth factor receptor modulator; cytosolic; cancer;

KM neoplasm; gene therapy; antisense therapy; antibody therapy;

XX drug screening; diagnosis; enzyme.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Domain 393..678 /note="inositol polyphosphate kinase domain"

XX WO2005072475-A2.

XX 11-AUG-2005.

XX 27-JAN-2005; 2005WO-US003560.

XX 28-JAN-2004; 2004US-0539837P.

XX (EXEL-) EXELIXIS INC.

XX Friedman L, Francis-Iang H, Parks AL, Shaw KJ, Bjerke LM;

XX Heuer TS;

XX WPI; 2005-555620/56.

XX N-PSDB; AEB87639.

XX REFSEQ; NP\_079470.

XX Identifying candidate Insulin Growth Factor Receptor pathway modulating

XX agents useful for diagnosing or treating, for e.g. cancer, comprises

XX triphosphate 3-kinase.

XX Disclousure; SEQ ID NO 10; 87bp; English.

XX The present sequence is the protein sequence of human inositol-

XX triphosphate 3-kinase C (ITPKC). A dominant loss of function screening

XX was carried out in Drosophila to identify genes that interact with or

XX modulate the insulin-like growth factor receptor (IGFR) signaling

XX pathway. Modifiers of the IGFR pathway were isolated, and the human

CC orthologs of these modifiers were identified as ITPKs. The invention

CC provides methods for using these IGFR modifier genes and polypeptides to

CC identify ITPK-modulating agents that are candidate therapeutic agents for

CC use in the treatment of disorders associated with defective or impaired

CC IGF function and/or ITPK function. In one embodiment, candidate ITPK

CC modulator agents are tested in an assay system comprising an ITPK

CC polypeptide or nucleic acid. Agents that produce a change in the activity

CC of the assay system relative to controls are identified as candidate IGFR

CC modulating agents. The screening assay system may be a binding assay, an

CC apoptosis assay, a cell proliferation assay, an angiogenesis assay or a

CC hypoxic induction assay. Preferred ITPK-modulating agents include small

CC molecule modulators, nucleic acid molecules such as antisense oligomers

CC or phosphorothioate morpholino oligomers, and antibodies. A probe for

CC ITPK expression is used in a claimed method for diagnosing a disease,

CC particularly cancer.

XX Sequence 683 AA;

QY 1 AVTKRYMQWRETMSTSTLGFRLEGIKKADGTCNTNFKKTOALEQYTKVLEDFVDDHV 60

DB 531 AVTKRYMQWRETMSTSTLGFRLEGIKKADGTCNTNFKKTOALEQYTKVLEDFVDDHV 590

QY 61 ILQKYVACLEBELRALISPEFKTHEVVGSSLLFVHDHTGLAKYWMIDFGKTVALPDHQT 120

DB 591 ILQKYVACLEBELRALISPEFKTHEVVGSSLLFVHDHTGLAKYWMIDFGKTVALPDHQT 650

QY 121 LSHRLPWAEGNREDGYL 137

DB 651 LSHRLPWAEGNREDGYL 667

RESULT 8

ID AAM41393 standard; protein; 687 AA.

AC AAM41393;

DT 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 6324.

XX Human, noctropic; immunosuppressant; cytosolic; gene therapy; cancer;

KM peripheral nervous system; neuropathy; central nervous system; CNS;

KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KM chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

XX leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-0052317.

XX 20-JUN-2000; 2000US-00588042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX  
DR MPI: 2001-442253/47.  
XX N-PSDB; AA160549.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
PS Example 2; SEQ ID NO 6324; 10078bp; English.  
XX  
CC The invention relates to human nucleic acids (AA157798-AA161369) and the  
CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localized neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 687 AA;  
XX  
Query Match 100.0%; Score 725; DB 4; Length 687;  
Best Local Similarity 100.0%; Pred. No. 5.8e-74;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 AATKRRYQMRRTMSSTLTGFRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVDDGHV 60  
DB 535 AATKRRYQMRRTMSSTLTGFRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVDDGHV 594  
XX  
QY 61 ILQKTVACLEELREALEISPPFKTHEVVGSSLLFVHDHTGLAKVMWIDFGKTVALLPDHOT 120  
DB 595 ILQKTVACLEELREALEISPPFKTHEVVGSSLLFVHDHTGLAKVMWIDFGKTVALLPDHOT 654  
XX  
QY 121 LSHRLPMAEGNREDGYL 137  
DB 655 LSHRLPMAEGNREDGYL 671  
XX  
Db  
XX  
RESULT 9  
AAM39607  
ID AAM39607 standard; protein; 711 AA.  
XX  
AC AAM39607;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 2752.  
XX  
XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
XX OS Homo sapiens.  
XX  
XX WO200153312-A1.  
XX  
XX PD 26-JUL-2001.  
XX  
XX PF 26-DEC-2000; 2000MO-US034263.  
XX  
XX PR 23-DEC-1999; 99US-00471275.  
XX  
XX PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
XX (HSE-) HSEQ INC.  
XX  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren P, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX  
DR MPI: 2001-442253/47.  
XX N-PSDB; AA158763.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
PS Example 4; SEQ ID NO 2752; 10078bp; English.  
XX  
CC The invention relates to human nucleic acids (AA157798-AA161369) and the  
CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localized neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 711 AA;  
XX  
Query Match 100.0%; Score 725; DB 4; Length 711;  
Best Local Similarity 100.0%; Pred. No. 6.1e-74;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 AATKRRYQMRRTMSSTLTGFRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVDDGHV 60  
DB 559 AATKRRYQMRRTMSSTLTGFRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVDDGHV 618  
XX  
QY 61 ILQKTVACLEELREALEISPPFKTHEVVGSSLLFVHDHTGLAKVMWIDFGKTVALLPDHOT 120  
DB 619 ILQKTVACLEELREALEISPPFKTHEVVGSSLLFVHDHTGLAKVMWIDFGKTVALLPDHOT 678  
XX  
QY 121 LSHRLPMAEGNREDGYL 137  
DB 679 LSHRLPMAEGNREDGYL 695  
XX  
Db  
XX  
RESULT 10  
ABB09772  
ID ABB09772 standard; protein; 461 AA.  
XX  
AC ABB09772;  
XX  
DT 22-JUL-2002 (first entry)  
XX  
XX Amino acid sequence of human inositol-1,4,5-triphosphate 3 kinase-A.  
XX  
XX IP3 kinase; inositol-1,4,5-triphosphate kinase; enzyme; oxidative stress;  
KW endoplasmic reticulum stress; neurodegeneration; retina; free radical;  
KW chronic infection; arthritis; cancer; cystic fibrosis;  
KW Alzheimer's disease; Huntington's disease; pigmentary retinopathy;  
KW DIP3X1, DIP3K2.  
XX

OS Homo sapiens.  
 XX FR2813612-A1.  
 XX  
 PD 08-MAR-2002.  
 XX  
 PF 07-SEP-2000; 2000FR-00011397.  
 XX  
 PR 07-SEP-2000; 2000FR-00011397.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PI Tricoire H, Monnier V, Pret AM, Cabet DE, Brissard J, Vandurka P,  
 PI Girardot F;  
 DR WPI: 2002-260343/31.  
 DR N-PSDB; ABL56444.  
 XX  
 PT New proteins with inositol-triphosphate kinase activity, useful e.g. for  
 PT treating oxidative stress and neurodegeneration.  
 XX  
 PS Claim 4; Fig 3; 69pp; French.  
 XX  
 CC The present sequence represents inositol-1,4,5-triphosphate 3 (IP3)  
 CC kinase-A protein. The specification also describes Drosophila IP3 kinase  
 CC proteins, designated DIP3K1 and DIP3K2. This protein has IP3 (inositol-  
 CC 1,4,5-triphosphate) kinase activity. The specification describes the use  
 CC of IP3 kinase proteins to prepare compositions for treating diseases  
 CC associated with oxidative stress, stress of the endoplasmic reticulum or  
 CC neurodegeneration, particularly of the retina. Overexpression of IP3  
 CC kinase protects cells against the damaging effects of free radicals  
 CC without altering free radical homeostasis within the cell. The IP3  
 CC proteins are used for treating disorders associated with oxidative  
 CC stress, stress on the endoplasmic reticulum and neurodegeneration,  
 CC particularly chronic infection (such as arthritis and some forms of  
 CC cancer), cystic fibrosis, Alzheimer's and Huntington's diseases, and  
 CC pigmentary retinopathy. Transgenic animals that lack the gene for IP3  
 CC kinase proteins are used to identify phenotypic alterations associated  
 CC with loss of this gene  
 XX  
 SQ Sequence 461 AA;  
 XX  
 Query Match 69.5%; Score 504; DB 5; Length 461;  
 Best Local Similarity 66.4%; Pred. No. 9.4e-49;  
 Matches 91; Conservative 22; Mismatches 24; Indels 0; Gaps 0;  
 QY 1 AVTKPRYQWQREMTSSTSLGFRLEGIKKADGTCNTNFKTKQALQVTKVLEDPVGDHV 60  
 DB 309 AVTKPRYQWQREMGSSSTTLGFRLEGIKKADGSCSTDFKTRSRQVLRVEEFGQDDE 368  
 QY 61 ILQKYVACLEELREALISPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTVALLPDHQT 120  
 DB 369 VLRRYLRNLQOIRLQTLSEFFRRHREVGSSLLFVHDHCHAGVWLIDFGKTVLPDQI 428  
 QY 121 LSHRLPMAEGNREDGYL 137  
 DB 429 LDHRRPMEEGNREDGYL 445  
 XX  
 RESULT 11  
 ADO44008  
 ID ADO44008 standard; protein; 461 AA.  
 XX  
 AC ADO44008;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Amino acid sequence of human ID-MYO-inositol triphosphate 3 kinase A.  
 XX  
 KW protein complex; neurological disease; stroke; neurodegeneration;  
 KW Wallerian degeneration; Alzheimer's disease; neurological disorder;  
 KW epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease;  
 KW atherosclerosis; ID-MYO-inositol triphosphate 3 kinase A; ASK1; ASK2;

KW ASK3; CAMKII beta; CAMKII delta; CAMKII gamma; casein kinase II alpha;  
 KW Cdc37; CHK2; CTCL tumour antigen SE20-4; EF-1 alpha 1; EMAP;  
 KW FLJ14653 NT2RP2002252; FLJ30839 PEBRA2002429; HERC2;  
 KW inositol polyphosphate-5-phosphatase; inositol-1; 4;  
 KW 5-triphosphate 5-phosphatase type 1; IRAK1; IRAK4; KIAA1441; MSTP030;  
 KW Nek9; PAR3; Pellino 1; Pellino 3; podocalyxin-like protein 1 precursor;  
 KW Pushover; S-adenosylhomocysteinease;  
 KW secretory carrier-associated membrane protein 2; surfactant locus protein 2;  
 KW ubiquitin carboxyl terminal hydrolase 11;  
 KW upstream regulatory element binding protein 1; Vartul;  
 KW Werner's syndrome helicase interacting protein; WHIP;  
 KW X-ray repair cross complementing protein 4.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004031242-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 11-SEP-2003; 2003WO-EP010110.  
 XX  
 PR 12-SEP-2002; 2002EP-00020495.  
 PR 12-SEP-2002; 2002EP-00020496.  
 PR 12-SEP-2002; 2002EP-00020497.  
 XX  
 PA (CELL-) CELLZOME AG.  
 XX  
 PI Bouwmeester T, Drewes G, Jackson D, Heltenbein G, Schirle M;  
 PI Kuester B, Hopf C;  
 DR WPI: 2004-316467/29.  
 XX  
 DR New complex comprising at least one first protein, and at least one  
 PT second protein, useful for treating stroke, Alzheimer's disease,  
 PT neurological disorders such as epilepsy, and inflammatory conditions such  
 PT as ulcerative colitis.  
 XX  
 PS Example; Page 243-245; 287pp; English.  
 XX  
 CC The specification describes protein complexes involved in cellular  
 CC processes which have been shown to be critical for the development of  
 CC various forms of neurological diseases. Three protein complexes were  
 CC identified: ASK2 protein complex, Pellino-1 protein complex and Pellino-3  
 CC protein complex. The protein complex are useful for treating diseases and  
 CC disorders, e.g. stroke, neurodegeneration such as Wallerian degeneration,  
 CC Alzheimer's disease, neurological disorders such as epilepsy, and  
 CC inflammatory conditions such as ulcerative colitis, Crohn's disease or  
 CC atherosclerosis. Proteins identified as being part of the protein  
 CC complexes of the invention are ID-MYO-inositol triphosphate 3 kinase A,  
 CC ASK1, ASK2, ASK3, CAMKII beta, CAMKII delta, CAMKII gamma, casein kinase  
 CC II alpha, Cdc37, CHK2, CTCL tumour antigen SE20-4, EF-1 alpha 1, EMAP,  
 CC FLJ14653 NT2RP2002252, FLJ30839 PEBRA2002429, HERC2, two hypothetical  
 CC proteins of 35.5 kDa and 49.3 kDa, inositol polyphosphate-5-phosphatase,  
 CC inositol-1,4,5-triphosphate 5-phosphatase type 1, IRAK1, IRAK4, KIAA1441,  
 CC MSTP030, Nek9, Pellino 1, Pellino 3, podocalyxin-like protein 1  
 CC precursor, Pushover, a putative S-adenosylhomocysteinease, secretory  
 CC carrier-associated membrane protein 2, surfactant locus protein 2, ubiquitin  
 CC carboxyl terminal hydrolase 11, upstream regulatory element binding  
 CC protein 1, Vartul, Werner's syndrome helicase interacting protein (WHIP),  
 CC X-ray repair cross complementing protein 4 (isoform 1). The present  
 CC sequence represents ID-MYO-inositol triphosphate 3 kinase A.  
 XX  
 SQ Sequence 461 AA;  
 XX  
 Query Match 69.5%; Score 504; DB 8; Length 461;  
 Best Local Similarity 66.4%; Pred. No. 9.4e-49;  
 Matches 91; Conservative 22; Mismatches 24; Indels 0; Gaps 0;  
 QY 1 AVTKPRYQWQREMTSSTSLGFRLEGIKKADGTCNTNFKTKQALQVTKVLEDPVGDHV 60  
 DB 309 AVTKPRYQWQREMGSSSTTLGFRLEGIKKADGSCSTDFKTRSRQVLRVEEFGQDDE 368  
 QY 61 ILQKYVACLEELREALISPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTVALLPDHQT 120



DB 369 VLRRYLNRLQGIROTLSEVSEFFRRHREIVGSSLLFVHDCHRAGVWLIDFGKTTPLPDQI 428  
 QY 121 LSHRLPMAEGNREDGYL 137  
 DB 429 LDHRRPMEEGNREDGYL 445

RESULT 12  
 AEB87636  
 ID AEB87636 standard; protein; 461 AA.  
 XX AEB87636;  
 AC AEB87636;  
 XX  
 DT 20-OCT-2005 (first entry)  
 XX  
 DE Human inositol-trisphosphate 3-kinase A (ITPKA).  
 XX  
 KW Inositol-trisphosphate 3-kinase A; ITPKA;  
 KW inulin-like growth factor receptor modulator; cytosolic; cancer;  
 KW neoplasm; gene therapy; antisense therapy; antibody therapy;  
 KW drug screening; diagnosis; enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 Key Location/Qualifiers  
 FH 171..456  
 FT Domain /note="Inositol polypophosphate kinase domain"  
 FT  
 XX  
 PN WO2005072475-A2.  
 XX  
 PD 11-AUG-2005.  
 XX  
 PF 27-JAN-2005; 2005WO-US003560.  
 XX  
 PR 28-JAN-2004; 2004US-0539837P.  
 XX  
 PA (EXEL-) EXELIXIS INC.  
 XX  
 PI Friedman L, Francis-Lang H, Parks AL, Shaw KJ, Björke LM;  
 PI Heuer TS;  
 XX  
 DR WPI; 2005-555620/56.  
 DR N-PSDB; AEB87629, AEB87630.  
 DR  
 XX REPEREQ; NP\_002211.  
 DR  
 PT Identifying candidate Insulin Growth Factor Receptor pathway modulating  
 PT agents useful for diagnosing or treating, for e.g. cancer, comprises  
 PT screening for agents that modulate the activity of Inositol 1,4,5-  
 PT triphosphate 3-kinase.  
 XX  
 PS Disclosure; SEQ ID NO 8; 87bp; English.  
 XX  
 CC The present sequence is the protein sequence of human inositol-  
 CC triphosphate 3-kinase A (ITPKA). A dominant loss of function screening  
 CC was carried out in *Drosophila* to identify genes that interact with or  
 CC modulate the inulin-like growth factor receptor (IGFR) signaling  
 CC pathway. Modifiers of the IGFR pathway were isolated, and the human  
 CC orthologs of these modifiers were identified as ITPKs. The invention  
 CC provides methods for using these IGFR modifier genes and polypeptides to  
 CC identify ITPK-modulating agents that are candidate therapeutic agents for  
 CC use in the treatment of disorders associated with defective or impaired  
 CC IGFR function and/or ITPK function. In one embodiment, candidate ITPK  
 CC modulator agents are tested in an assay system comprising an ITPK  
 CC polypeptide or nucleic acid. Agents that produce a change in the activity  
 CC of the assay system relative to controls are identified as candidate IGFR  
 CC modulating agents. The screening assay system may be a binding assay, an  
 CC apoptosis assay, a cell proliferation assay, an angiogenesis assay, an  
 CC hypoxic induction assay. Preferred ITPK-modulating agents include small  
 CC molecule modulators, nucleic acid molecules such as antisense oligomers  
 CC or phosphorochioate morpholino oligomers, and antibodies. A probe for  
 CC ITPK expression is used in a claimed method for diagnosing a disease,  
 CC particularly cancer.

XX  
 SQ Sequence 461 AA;  
 Query Match 69.5%; Score 504; DB 9; Length 461;  
 Best Local Similarity 66.4%; Pred. No. 9.4e-49;  
 Matches 91; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 1 AVTKPRYQWRETNSTSTLGRIGIKKADGTCNTNFKTQALRQVTKLEDPVGDHV 60  
 DB 309 AVTKPRYQWRETNSTSTLGRIGIKKADGSCSTDKTKTRSRQVLRVEEFOQSDDE 368  
 QY 61 ILQKTVACLEERLEALRISPFKTEHVGVSSLLFVHDTGLAKVMMDPGKTVAPDDQT 120  
 DB 369 VLRRYLNRLQGIROTLSEVSEFFRRHREIVGSSLLFVHDCHRAGVWLIDFGKTTPLPDQI 428  
 QY 121 LSHRLPMAEGNREDGYL 137  
 DB 429 LDHRRPMEEGNREDGYL 445

RESULT 13  
 ABB09782  
 ID ABB09782 standard; protein; 477 AA.  
 XX  
 AC ABB09782;  
 XX  
 DT 22-JUL-2002 (first entry)  
 XX  
 DE Amino acid sequence of human inositol-1,4,5-trisphosphate 3 kinase-A.  
 XX  
 KW IP3 kinase; inositol-1,4,5-trisphosphate kinase; enzyme; oxidative stress;  
 KW endoplasmic reticulum stress; neurodegeneration; retina; free radical;  
 KW chronic infection; arthritis; cancer; cystic fibrosis;  
 KW Alzheimer's disease; Huntington's disease; pigmentary retinopathy;  
 KW DIP3K1; DIP3K2.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200220742-A1.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 31-AUG-2001; 2001WO-FR002708.  
 XX  
 PR 07-SEP-2000; 2000FR-00011397.  
 XX  
 PA (CNRS ) CENT NAT RECH SCI.  
 XX  
 PI Tricolre H, Monnier V, Pret A, Busson DE, Zahraoui J, Vandurka P;  
 PI Girardot F;  
 XX  
 DR WPI; 2002-260343/31.  
 DR  
 XX  
 PT New proteins with inositol-trisphosphate kinase activity, useful e.g. for  
 PT treating oxidative stress and neurodegeneration.  
 XX  
 PS Claim 4; Page 53-54; 64bp; French.  
 XX  
 CC The present sequence represents inositol-1,4,5-trisphosphate 3 (IP3)  
 CC kinase-A protein. The specification also describes *Drosophila* IP3 kinase  
 CC proteins, designated DIP3K1 and DIP3K2. This protein has IP3 (inositol-  
 CC 1,4,5-trisphosphate) kinase activity. The specification describes the use  
 CC of IP3 kinase proteins to prepare compositions for treating diseases  
 CC associated with oxidative stress, stress of the endoplasmic reticulum or  
 CC neurodegeneration, particularly of the retina. Overexpression of IP3  
 CC kinase protects cells against the damaging effects of free radicals  
 CC without altering free radical homeostasis within the cell. The IP3  
 CC proteins are used for treating disorders associated with oxidative  
 CC stress, stress on the endoplasmic reticulum and neurodegeneration,  
 CC particularly chronic infection (such as arthritis and some forms of  
 CC cancer); cystic fibrosis; Alzheimer's and Huntington's diseases, and  
 CC pigmentary retinopathy. Transgenic animals that lack the gene for IP3  
 CC kinase proteins are used to identify phenotypic alterations associated



CC cancer); cystic fibrosis; Alzheimer's and Huntington's diseases, and  
 CC pigmentary retinopathy. Transgenic animals that lack the gene for IP3  
 CC kinase proteins are used to identify phenotypic alterations associated  
 CC with loss of this gene. This specification is equivalent to FR2813612  
 XX

SQ Sequence 472 AA;

Query Match 68.0%; Score 493; DB 5; Length 472;  
 Best Local Similarity 67.9%; Pred. No. 1.8e-47;  
 Matches 93; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

QY 1 AVTKPRYMQWRETMSSTSTLGFRIKADGTCNTNFKKTOALBQVTKVLEDFVGDHV 60  
 |||||  
 Db 316 AVTKPRYMQWRETISSTATLGFRIKEDGTNRDFKKTREQVTEAFREFTKGNHN 375  
 61 ILQKVVACLEBELREALETSPFKEHVVGSLLFVHDHGLAKWMMIDRGKTVALPDHOT 120  
 |||||  
 Db 376 ILIAYRDRILKAIKRTTLBVSFFPKCHVIGSSLLFTHDKKQAKVWMDPGKTTPLPEGQT 435  
 121 LSHRLPMAEGNREDGYL 137  
 |||||  
 Db 436 LQHDVPMQEGNREDGYL 452

Search completed: May 21, 2006, 04:20:23  
 Job time : 196 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: May 21, 2006, 04:20:44 ; Search time 38 Seconds  
(without alignments)  
346.887 Million cell updates/sec

Title: US-10-781-581-226

Perfect score: 725

Sequence: 1 AVTKPRYQMREMTSSTL.....HQTLSRLPMAGNRDGYL 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	506	69.8	459	2	SI3064
2	504	69.5	461	2	JN0129
3	493	68.0	472	2	SI7682
4	493	68.0	946	2	UC7810
5	487	67.2	673	2	SI4053
6	321	44.3	394	2	T42512
7	321	44.3	461	2	T42512
8	321	44.3	486	2	T25639
9	321	44.3	494	2	T42444
10	90	12.4	268	2	T50224
11	78	10.8	555	2	T32105
12	77.5	10.7	476	2	T27707
13	77.5	10.7	775	2	K70320
14	76	10.5	1047	2	A12002
15	75	10.3	302	2	H86391
16	74.5	10.3	338	2	A81422
17	74.5	10.3	922	2	AG1827
18	74	10.2	249	2	H90048
19	74	10.2	288	2	H87642
20	74	10.2	912	2	T19961
21	73.5	10.1	361	2	AC1437
22	73.5	10.1	607	2	G84630
23	73	10.1	356	2	C70398
24	73	10.1	810	2	T45679
25	72.5	10.0	349	2	A72750
26	72.5	10.0	362	2	A64212
27	72.5	10.0	625	2	DB6903
28	72	9.9	467	2	T55848
29	72	9.9	602	1	T35760

30	71.5	9.9	715	2	B75135	DNA helicase relat
31	71.5	9.9	807	2	E90523	leucyl-tRNA synthet
32	71	9.8	205	2	AB1903	hypothetical prote
33	71	9.8	427	2	SS7776	cysteine proteinase
34	71	9.8	430	2	QJ0120	hypothetical prote
35	71	9.8	1446	2	T30916	carboxypeptidase D
36	71	9.8	2137	1	SNHUB	spectrin beta chain
37	70.5	9.7	366	1	A46704	aryl-alcohol dehyd
38	70.5	9.7	497	2	E96774	probable cytochrom
39	70.5	9.7	640	1	VCNVRV	env polyprotein pr
40	70.5	9.7	676	1	VCNVRV	env polyprotein pr
41	70.5	9.7	967	2	T41672	probable b-zip tra
42	70.5	9.7	2030	2	T33162	hypothetical prote
43	70	9.7	286	2	H86664	outer membrane lip
44	70	9.7	617	2	S37744	endo-exonuclease y
45	70	9.7	644	2	S15464	gp70 protein - mur

## ALIGNMENTS

## RESULT 1

SI3064  
ID-myo-inositol-trisphosphate 3-kinase (BC 2.7.1.127) A - rat  
N:Alternate names: inositol-1,4,5-trisphosphate 3-kinase  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: SI3064; A34854; S56747  
R:Takazawa, K.; Vandekerckhove, J.; Dumont, J.E.; Erneux, C.  
Biochem. J. 272, 107-112, 1990  
A:Title: Cloning and expression in Escherichia coli of a rat brain cDNA encoding a Ca(2+  
A:Reference number: SI3064; MUID:91090700; PMID:2176078  
A:Accession: SI3064

A:Molecule type: mRNA

A:Residues: 1-459 <TK>

A:Cross-references: UNIPROT:P17105; UNIPARC:UPI000012D7C2; GB:X56917; NID:G56388; PIDN:C

A:Experimental source: brain

R:Choi, K.Y.; Kim, H.K.; Lee, S.Y.; Moon, K.H.; Sim, S.S.; Kim, J.W.; Chung, H.K.; Rhee,

Science 248, 64-66, 1990

A:Title: Molecular cloning and expression of a complementary DNA for inositol 1,4,5-tris

A:Reference number: A34854; MUID:90208336; PMID:2157285

A:Accession: A34854

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 10-459 <CHO>

A:Cross-references: UNIPARC:UPI00001679B7; GB:M29787; NID:G204987; PIDN:AAA41457.1; PID:

A:Experimental source: brain

R:Communi, D.; Lecocq, R.; Vanweyenbergh, V.; Erneux, C.

Biochem. J. 310, 109-115, 1995

A:Title: Active site labelling of inositol 1,4,5-trisphosphate 3-kinase A by phenylglyox

A:Reference number: S56747; MUID:95374430; PMID:7646431

A:Accession: S56747

A:Molecule type: protein

A:Residues: 315-326 <COM>

A:Cross-references: UNIPARC:UPI0000179A9C

A:Experimental source: brain

C:Function:

A:Description: catalyzes the phosphorylation of inositol-1,4,5-trisphosphate to inositol-1

C:Keywords: brain; phosphoprotein; phosphotransferase

F:119/Binding site: phosphate (Ser) (covalent) (by cAMP- and calmodulin-dependent kinase

F:119/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F:309/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #status

F:346/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 69.8%; Score 506; DB 2; Length 459;

Best Local Similarity 67.2%; Pred. No. 3.3e-40;

Matches 92; Conservative 22; Mismatches 23; Indels 0; Gaps 0;

OY 1 AVTKPRYQMREMTSSTLGGFRLEGKXKADGTNTNPKTKQALQYTKLVEDVGDHV 60  
DB 307 AVTKPRYQMREMTSSTLGGFRLEGKXKADGTNTNPKTKQALQYTKLVEDVGDHV 60  
OY 61 ILQYVACLEELRALALISPPFKTHREVVGSLFVVDHDTGLAKYMMIDFGTVALPBDQT 120

Db 367 VLKRYLNRLOQIRDTLEISDFRRHEVIGSSLLFVHDHCHRAQVWLLIDFGKTPPLPDQGI 426  
QY 121 LSHRLPWAEGNREGDYL 137  
Db 427 LDHRRPWEENREGDYL 443

## RESULT 2

JN0129  
ID-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) A - human  
N/Alternate names: inositol-1,4,5-trisphosphate 3-kinase A  
C/Species: Homo sapiens (man)  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C/Accession: JN0129; S13559  
R/Takazawa, K.; Perret, J.; Dumont, J.E.; Erneux, C.  
Biochem. Biophys. Res. Commun. 174, 529-535, 1991  
A/Title: Molecular cloning and expression of a human brain inositol 1,4,5-trisphosphate  
A/Reference number: JN0129; MUID:91128380; PMID:1847047  
A/Accession: JN0129  
A/Molecule type: mRNA  
A/Residues: 1-461 <TRK1>  
A/Cross-references: UNIPROT:P23677; UNIPARC:UPI000049A1A; EMBL:X54938; NID:932104; PID:  
R/Takazawa, K.; Perret, J.; Dumont, J.E.; Erneux, C.  
Nucleic Acids Res. 18, 7141, 1990  
A/Title: Human brain inositol 1,4,5-trisphosphate 3-kinase cDNA sequence.  
A/Reference number: S13559; MUID:91088302; PMID:2175886  
A/Accession: S13559  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-461 <TRK2>  
A/Cross-references: UNIPARC:UPI000049A1A; EMBL:X54938; NID:932104; PID:CAA38700.1; PID:  
C/Genetics:  
A/Gene: GDB:ITPKA  
A/Cross-references: GDB:126863; OMIM:147521  
A/Map position: 15q15.1-15q21.1  
C/Function:  
A/Description: catalyzes the phosphorylation of inositol-1,4,5-trisphosphate to inositol-  
A/Keywords: phosphoprotein; phosphorylation  
F/11/Binding site: phosphate (Ser) (covalent) (by CAMP- and calmodulin-dependent kinase  
F/117/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F/311/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #stat  
F/348/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
Query Match 69.5%; Score 504; DB 2; Length 461;  
Best Local Similarity 66.4%; Pred. No. 5.2e-40;  
Matches 91; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

A/Molecule type: mRNA  
A/Residues: 1-472 <TRK>  
A/Cross-references: UNIPARC:UPI000049A1B; EMBL:X57206; NID:933990; PID:CAA40491.1; PID:  
C/Genetics:  
A/Gene: GDB:ITPKB  
A/Cross-references: GDB:128973; OMIM:147522  
A/Map position: 1q41-1q43  
A/Keywords: phosphotransferase  
Query Match 68.0%; Score 493; DB 2; Length 472;  
Best Local Similarity 67.9%; Pred. No. 5.9e-39;  
Matches 93; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

QY 1 AVTKPRYMQWRETMSSTSLGFRLEGIKKADGTCNTNFKKTQALEQVTKVLEDFVGDHV 60  
Db 316 AVTKPRYMQWRETMSSTSLGFRLEGIKKEDGTVNRPFKTKTREQVTEAFREFTKGNHN 375  
QY 61 ILQKYVACLEBRLALEISPFKTHEVVGSSLLFVHDHGLAKYWMIDFGKTVALLPDHOT 120  
Db 376 ILIAYRDLKAIKRTTLEVSFPFKCHEVIGSSLLFIHDKKEQAKYWMIDFGKTPPLPDQOT 435  
QY 121 LSHRLPWAEGNREGDYL 137  
Db 436 LDHVPWQEGNREGDYL 452

## RESULT 4

JC7810  
inositol 1,4,5-trisphosphate 3-kinase B - human  
C/Species: Homo sapiens (man)  
C/Date: 03-Jun-2002 #sequence\_revision 03-Jun-2002 #text\_change 03-Jun-2002  
C/Accession: JC7810  
R/Dewaste, V.; Roymans, D.; Moreau, C.; Erneux, C.  
Biochem. Biophys. Res. Commun. 291, 400-405, 2002  
A/Title: Cloning and expression of a full-length cDNA encoding human inositol 1,4,5-trisph  
A/Reference number: JC7810; PMID:11846419; MUID:21835501  
A/Contents: Frontal cortex  
A/Accession: JC7810  
A/Molecule type: mRNA  
A/Residues: 1-946 <DEM>  
A/Cross-references: UNIPARC:UPI000017CD41; GB:Y18024  
C/Comment: This enzyme, an isoenzyme of inositol 1,4,5-trisphosphate (Ino3P) 3-kinase, ca  
of calcium homeostasis. This enzyme is particularly sensitive to Ca2+ in the presence of

Query Match 68.0%; Score 493; DB 2; Length 946;  
Best Local Similarity 67.9%; Pred. No. 1.3e-38;  
Matches 93; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

QY 1 AVTKPRYMQWRETMSSTSLGFRLEGIKKADGTCNTNFKKTQALEQVTKVLEDFVGDHV 60  
Db 309 AVTKPRYMQWREGSSSTSLGFRLEGIKKADGSCSTDFTKTRSRQVLRVPEEFVQGDDE 368  
QY 61 ILQKYVACLEBRLALEISPFKTHEVVGSSLLFVHDHGLAKYWMIDFGKTVALLPDHOT 120  
Db 369 VLRRYLRNLQOIRLTLEVSFPFKCHEVIGSSLLFVHDHCHRAQVWLLIDFGKTPPLPDQOI 428  
QY 121 LSHRLPWAEGNREGDYL 137  
Db 429 LDHRRPWEENREGDYL 445

## RESULT 3

S17682  
ID-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) B - human  
N/Alternate names: inositol-1,4,5-trisphosphate 3-kinase B  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jul-2000  
C/Accession: S17682  
R/Takazawa, K.; Perret, J.; Dumont, J.E.; Erneux, C.  
Biochem. J. 278, 883-886, 1991  
A/Title: Molecular cloning and expression of a new putative inositol 1,4,5-trisphosphate  
A/Reference number: S17545; MUID:91378954; PMID:1654894  
A/Accession: S17682

## RESULT 5

S41053  
ID-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) B - rat  
N/Alternate names: IP(3) 3-kinase  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S41053; S54349; S35963  
R/Thomas, S.; Brake, B.; Luzzio, J.P.; Stanley, K.; Banting, G.  
Biochem. Biophys. Acta 1220, 219-222, 1994  
A/Title: Isolation and sequence of a full length cDNA encoding a novel rat inositol 1,4,5-  
A/Reference number: S41053; MUID:94146119; PMID:83123366  
A/Accession: S41053







E70320  
polyribonucleotide nucleotidyltransferase - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C:Accession: E70320  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov  
V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196666; PMID:9537320  
A:Accession: E70320  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-775 <AOF>  
A:Cross-references: UNIPROT:Q66593; UNIPARC:UPI00000562CC; GB:AE000679; NID:92982936; PI  
A:Experimental source: strain VFS  
C:Genetics:  
A:Gene: phpA  
C:Superfamily: polyribonucleotide nucleotidyltransferase

Query Match 10.7%; Score 77.5; DB 2; Length 775;  
Best Local Similarity 26.9%; Pred. No. 26;  
Matches 35; Conservative 23; Mismatches 43; Indels 29; Gaps 7;

Oy 4 KPRYQMEETMSSTSLG---FRIGIKKADGTCNTNPKTQALRQVTK-----VLEDPV 55  
Db 473 KDRYVILSDIIGDEBDHLGDMDFKVGTK--DGI--TSVQMDIKVIGITKEIMLDLKKAR 528  
Oy 56 DGDHYILQKYVACLEELREALISPPFKTHEVY-----GSSLLFVHDHGL 101  
Db 529 EGRYLILKMYEALPEPRK--BPHYTPRVAVDVPEKAPLLIGPGSTVKKIYDETV 586

Oy 102 AKVMWIDFGK 111  
Db 587 -KVMWGEQK 595

RESULT 14  
A12002  
hypotheical protein alr1575 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: A12002  
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Itiguchi,  
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tadota, S  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: A12002  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1047 <KUR>  
A:Cross-references: UNIPROT:Q8YVNO; UNIPARC:UPI00000CE131; GB:BA000019; PIDN:BA077941.1;  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr1575

Query Match 10.5%; Score 76; DB 2; Length 1047;  
Best Local Similarity 25.2%; Pred. No. 50;  
Matches 32; Conservative 17; Mismatches 44; Indels 34; Gaps 7;

Oy 36 TNPKKT--QALEQVTKVLEDFVDGDHYILQKYVACLEELREALISPPFKT---HEVGS 90  
Db 477 TNFEQETIKGIESANNFL--FIISSPKSLSSPY--CTTEVEYAMNINKRIIVTLVREIRGA 532  
Oy 91 SLFVHDHDTGLAKVMWIDFG-----KTVALPDHQTLSH-----RLPMAEG 130  
Db 533 TL-----HPGLAKVQWIDFSGHNDPFLTKFGELTRTLSDPEYVASHTRIFLAKADWEEH 587  
Oy 131 NREDCYL 137  
Db 588 NRDSDFL 594

## RESULT 15

H86391  
hypotheical protein TIK7.13 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2004  
C:Accession: H86391  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Comn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: AB6141; MUID:21016719; PMID:11130712  
A:Accession: H86391  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-302 <STO>  
A:Cross-references: UNIPROT:Q9FZD5; UNIPARC:UPI00000A8E7F; GB:AE005172; NID:9797750; PI  
C:Genetics:  
A:Map position: 1  
C:Superfamily: hypotheical protein containing F-box domain

Query Match 10.3%; Score 75; DB 2; Length 302;  
Best Local Similarity 30.3%; Pred. No. 15;  
Matches 27; Conservative 11; Mismatches 31; Indels 20; Gaps 5;

Oy 50 VLEDVDDHYILQKYVACLEELREALISPPFKTHEVVGSSLLFVHDHDTGLAKW-MID 108  
Db 169 VKSFPGYDVPVSDYKSCWTERRRGLQDP--SSEHQVF-----TLSEKKPKWKMD 218  
Oy 109 FGKTVLPDHQTLSHRLPMAEGNREDCYL 137  
Db 219 ---CTSIDPDR-----PMSGVCIDGRV 238

Search completed: May 21, 2006, 04:26:09  
Job time : 40 secs

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein, Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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O9Y475_HUMAN PRELIMINARY; PRT; 604 AA.
ID O9Y475_HUMAN
AC O9Y475;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Inositol 1,4,5-trisphosphate 3-kinase isoenzyme (EC 2.7.1.127)
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxID=9606;
RN Nucleotide Sequence.
RP TISSUE=Thyroid gland;
RA Takazawa K., Go M., Togaishi S., Endo T., Ernoux C., Onaya T.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
EMBL: D88169; BAA23524.1; -; mRNA.
DR Ensembl: ENSG00000086544; Homo sapiens.
DR GO: GO:0008440; F:inositol trisphosphate 3-kinase activity; IEA.
DR GO: GO:0016301; F:kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR005522; IPK.
DR Pfam: PF03770; IPK; 1.
DR Kinase: Transferase. 1.
FT NON_TER
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Query Match 100.0%; Score 725; DB 2; Length 604;
Best Local Similarity 100.0%; Pred. No. 5.4e-60;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVTKPRYQMWRMTSSTSTLGFRIEGIKKADGTCNTNPFKKTQALEQVTKVLEDFVDDGHV 60
DB 452 AVTKPRYQMWRMTSSTSTLGFRIEGIKKADGTCNTNPFKKTQALEQVTKVLEDFVDDGHV 511
QY 61 ILQKYVACLBEALREALEISPFKTHEVVGSSLLFVHDHTGLAKWMIDFGKTVALPDHQT 120
DB 512 ILQKYVACLBEALREALEISPFKTHEVVGSSLLFVHDHTGLAKWMIDFGKTVALPDHQT 571
QY 121 LSHRLPWAEGNRBDGYL 137
DB 572 LSHRLPWAEGNRBDGYL 588
RESULT 3
O96DU7_HUMAN PRELIMINARY; PRT; 683 AA.
ID O96DU7_HUMAN
AC O96DU7;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Inositol 1,4,5-trisphosphate 3-kinase C.
GN Name=ITPKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxID=9606;
RN Nucleotide Sequence.
RP TISSUE=Thyroid;
RA MELINE=20539819; PubMed=11085927; DOI=10.1042/0264-6021.3520343;
RA Dewaere V., Pouillon V., Moreau C., Shears S., Takazawa K., Ernoux C.;
RT "Cloning and expression of a cDNA encoding human inositol 1,4,5-
RL Biochem. J. 352:343-351(2000).
[2]

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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshilyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywiński M.I., Skalačka U., Smalins D.E.,
RA Schmeckel A., Schein U.E., Jones S.U.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RG NIH WGC Project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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EMBL: AJ290975; CAC40815.1; -; mRNA.
DR Ensembl: BC060788; AAB60788.1; -; mRNA.
DR SMR: Q96DU7; 425-683.
DR Ensembl: ENSG00000086544; Homo sapiens.
DR HGNC: HGNC:14897; ITPKC.
DR GO: GO:0008440; F:inositol trisphosphate 3-kinase activity; IEA.
DR GO: GO:0016301; F:kinase activity; IEA.
DR InterPro: IPR005522; IPK.
DR Pfam: PF03770; IPK; 1.
DR Kinase.
SQ SEQUENCE 683 AA; 75207 MW; 58093A2A8E046458 CRC64;
Query Match 100.0%; Score 725; DB 2; Length 683;
Best Local Similarity 100.0%; Pred. No. 6.2e-60;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVTKPRYQMWRMTSSTSTLGFRIEGIKKADGTCNTNPFKKTQALEQVTKVLEDFVDDGHV 60
DB 531 AVTKPRYQMWRMTSSTSTLGFRIEGIKKADGTCNTNPFKKTQALEQVTKVLEDFVDDGHV 590
QY 61 ILQKYVACLBEALREALEISPFKTHEVVGSSLLFVHDHTGLAKWMIDFGKTVALPDHQT 120
DB 591 ILQKYVACLBEALREALEISPFKTHEVVGSSLLFVHDHTGLAKWMIDFGKTVALPDHQT 650
QY 121 LSHRLPWAEGNRBDGYL 137
DB 651 LSHRLPWAEGNRBDGYL 667
RESULT 4
Q80ZG2_RAT PRELIMINARY; PRT; 678 AA.
ID Q80ZG2_RAT
AC Q80ZG2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Inositol 1,4,5-trisphosphate 3-kinase C.
GN Name=Itpkc; Synonyms=Ip3k-C;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 21, 2006, 04:17:09 ; Search time 296 Seconds

(without alignments)  
428.132 Million cell updates/sec

Title: US-10-781-581-226

Sequence: 1 AVTFRYVQMEETMSSTL.....HOTSLRLPMAEGNRDGYL 137

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_crembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	725	100.0	137	Q9UE25_HUMAN	Q9UE25 homo sapien
2	725	100.0	604	Q9Y475_HUMAN	Q9Y475 homo sapien
3	725	100.0	683	Q96DU7_HUMAN	Q96DU7 homo sapien
4	660	91.0	678	Q80ZG2_RAT	Q80ZG2 rattus norv
5	658	90.8	678	Q3U384_MOUSE	Q3U384 mus musculu
6	658	90.8	678	Q7TS72_MOUSE	Q7TS72 mus musculu
7	524	72.3	300	Q4SP10_TETNG	Q4SP10 tetradon n
8	517	71.3	395	Q5RGF0_BRARE	Q5RGF0 brachydantio
9	514	70.9	452	Q9YH86_GALLI	Q9YH86 gallus galli
10	513	70.8	400	Q5XK93_XENLA	Q5XK93 xenopus lae
11	513	70.8	516	Q2TA84_XENLA	Q2TA84 xenopus lae
12	507	69.9	325	Q4SC34_TETNG	Q4SC34 tetradon n
13	506	69.8	425	Q4RM63_TETNG	Q4RM63 tetradon n
14	506	69.8	455	IP3KA_MOUSE	IP3KA mus musculu
15	506	69.8	459	IP3KA_HUMAN	IP3KA homo sapien
16	504	69.5	461	IP3KA_HUMAN	IP3KA homo sapien
17	496.5	68.5	298	Q8JFJ9_BRARE	Q8JFJ9 brachydantio
18	494.5	68.2	195	Q2TU82_HUMAN	Q2TU82 homo sapien
19	493	68.0	472	Q2TU82_HUMAN	Q2TU82 homo sapien
20	493	68.0	944	IP3KB_HUMAN	IP3KB homo sapien
21	487	67.2	936	IP3KB_RAT	IP3KB rattus norv
22	442	61.0	310	Q4S868_TETNG	Q4S868 tetradon n
23	434	59.9	282	Q73592_CHICK	Q73592 gallus galli
24	410.5	56.6	377	Q5TX95_ANOGA	Q5TX95 anopheles g
25	410.5	56.6	398	Q7PTK9_ANOGA	Q7PTK9 anopheles g
26	403.5	55.7	669	Q8XSX8_DROME	Q8XSX8 drosophila
27	403.5	55.7	669	Q9YVE6_DROME	Q9YVE6 drosophila
28	387	53.4	463	Q963D4_APIME	Q963D4 apis mellif
29	387	53.4	548	Q963D3_APIME	Q963D3 apis mellif
30	387	53.4	782	Q963D5_APIME	Q963D5 apis mellif
31	321	44.3	393	Q61HCS_CAEEL	Q61HCS caenorhabdi

32	321	44.3	394	2	Q45050_CAEEL	Q45050 caenorhabdi
33	321	44.3	394	2	Q95Q63_CAEEL	Q95Q63 caenorhabdi
34	321	44.3	461	2	Q45051_CAEEL	Q45051 caenorhabdi
35	321	44.3	461	2	Q9GYT6_CAEEL	Q9GYT6 caenorhabdi
36	321	44.3	494	2	Q45048_CAEEL	Q45048 caenorhabdi
37	321	44.3	494	2	Q95Q62_CAEEL	Q95Q62 caenorhabdi
38	316.5	43.7	308	2	Q5DHU6_SCHJA	Q5DHU6 schistosoma
39	259.5	35.8	441	2	Q95R55_DROME	Q95R55 drosophila
40	259.5	35.8	441	2	Q9VL83_DROME	Q9VL83 drosophila
41	246.5	34.0	305	2	Q7Q1X4_ANOGA	Q7Q1X4 anopheles g
42	129	17.8	172	2	Q9PM03_CHICK	Q9PM03 gallus galli
43	129	17.8	181	2	Q9PM02_CHICK	Q9PM02 gallus galli
44	90	12.4	268	2	Q9US14_SCHPO	Q9US14 schizosacch
45	86	11.9	569	2	Q2R2E6_ORYSA	Q2R2E6 oryza sativ

## ALIGNMENTS

## RESULT 1

Q9UE25\_HUMAN PRELIMINARY; PRT; 137 AA.

AC Q9UE25\_01-MAY-2000, integrated into UniprotKB/TrEMBL.

DT 01-MAY-2000, sequence version 1.

DE Inositol 1,4,5-trisphosphate 3-kinase (Fragment).

GN Name=Insp 3-kinase C;

OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Placenta;

RA Ertaux C., Communi D.;

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

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OC Muroidea; Muridae; Murinae; Rattus.  
 OK NCB1\_TaxID=10116;  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX MEDLINE=22651089; PubMed=12649294; DOI=10.1074/jbc.M211059200;  
 RA Nalaskowski M.M., Bettsch U., Fanick W., Stockebbrand M.C., Schmale H.,  
 RA May G.W.;  
 RT "Rat inositol 1,4,5-trisphosphate 3-kinase C is enzymatically  
 RT specialized for basal cellular inositol trisphosphate phosphorylation  
 RT and shuttles actively between nucleus and cytoplasm.",  
 RL J. Biol. Chem. 278:19765-19776(2003).  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Miscar; TISSUE=Circumvallate taste papilla;  
 RA Bettsch U., Schmale H., Deschermeier C., Christiansen H., Fanick W.,  
 RA May G.W.;  
 RL Submitted (ARR-2002) to the EMBL/GenBank/DBJ databases.  
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 DR EMBL; AY160770; AAC20335.1; -; mRNA.  
 DR EMBL; AJ440782; CAD29464.1; -; mRNA.  
 DR SRR; Q80262; 420-678.  
 DR Ensembl; ENSRNOC00000013945; Rattus norvegicus.  
 DR RGD; 631336; Itpkc.  
 DR GO; GO:0016301; P:kinase activity; IDA.  
 DR InterPro; IPR005522; IPK.  
 DR Pfam; PF03770; IPK; 1.  
 DR KMA.  
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 Best Local Similarity 92.0%; Pred. No. 9.2e-54;  
 Matches 126; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
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 DB 526 AVTKPRYQWQREBTWSSTSTLGFRIEIGIKADGTCTNPKTKQALEQVTKLEDFVQDGHV 585  
 QY 61 ILQKTVACLEBRLERLEISPPFKTHEVVGSSLLFVHDHTGLAKYWMIDFGKTVALLPDHQT 120  
 DB 586 ILKRVYARLEDLRLTLENSPFFKTHEVVGSSLLFVHDHTGLAKYWMIDFGKTVALLPDHQM 645  
 QY 121 LSHRLPWAEGNRDGYL 137  
 DB 646 LSHRLPWAEGNRDGYL 662  
 RESULT 5  
 ID Q3U384\_MOUSE PRELIMINARY; PRT; 678 AA.  
 AC Q3U384;  
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.  
 DT 07-FEB-2006, entry version 5.  
 DE NOD-derived CDLIC Ave dendritic cells cDNA, RIKEN full-length enriched  
 DE library, clone:630110023 product:inositol 1,4,5-trisphosphate 3-  
 DE kinase C, full insert sequence.  
 GN Name=Itpkc;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.",  
 RL Methods Enzymol. 303:19-44(1999).

RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodius R., Shimokawa K.,  
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
 RA Davis J.B., Wilming L.G., Aidinis V., Allen J.E.,  
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 RA Banal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 RA Crome M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
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 RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelsso J., Kitamura H.,  
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 RA Tammoya K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 RA Ueda H.R., van Nimwegen B., Verardo R., Wei C.L., Yang K.,  
 RA Yamashita H., Zdobych E., Zhu S., Zimmer A., Hide W., Bult C.,  
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
 RA Wahlestedt C., Watford J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
 RA Fukuoka S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida Y., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Nimomiya N.,  
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
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 RA Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome.",  
 RL Science 309:1559-1563(2005).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RA RIKEN Genome Exploration Research Group, and Genome Science Group  
 RA (Genome Network Core Team) and the PANTOM Consortium;  
 RT "Antisense Transcription in the Mammalian Transcriptome.",  
 RL Science 309:1564-1566(2005).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD;  
 RX MEDLINE=22354683; PubMed=12468851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaio I., Osato N., Saito K., Suzuki H., Yamano H., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Bruneis V., Choithia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Gaston-McCormick S., Gustincich S., Hirokawa N., Jackson I.D., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sadelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirokane K., Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arahata T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ND;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arahata T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirml L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
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 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mommaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
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 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ND;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ND;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama Y., Nishi K., Kitahara T., Tashiro H., Itoh M.,  
 RA Sumi M., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kasaiwaigi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 [8]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ND;  
 RA Arahata T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
 RA Hori F., Iida J., Imanura K., Imotani K., Itoh M., Kanagawa S.,  
 RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Ninomiya N.,  
 RA Nishiyori H., Nomura K., Ono M., Sakazume N., Sano H., Sasaki D.,  
 RA Shibata K., Shiraki T., Tagami Y., Waki K., Watanabe A.,  
 RA Muramatsu M., Hayashizaki Y.,  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
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 CC EMBL; AK154888; BAB32904.1; -, mRNA.

DR MGI; MGI:2442554; Itpkc.  
 DR GO; GO:0008440; F:inositol triphosphate 3-kinase activity; IDA.  
 DR InterPro; IPR005522; IPK.  
 DR Pfam; PF03770; IPK; 1.  
 DR Knaae.  
 SQ SEQUENCE 678 AA; 74492 MW; 61DFCB3F3CC6B807 CRC64;  
 Query Match 90.8%; Score 658; DB 2; Length 678;  
 Best Local Similarity 91.2%; Pred. No. 1,4e-53;  
 Matches 125; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 AVTKPRYMQWRETMSSTSLGFRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVNDGHV 60  
 DB 526 AITKPRYMQWRETSLSTSLGFRIGIKKADGTCNTNFKKTOALEQVTKVLEDFVNDGLG 585  
 QY 61 ILQKYACIELEALIEIPFKTHVVGSSLLFVNDHGLAKVMWIDGKTVLPDQOT 120  
 DB 586 ILKRYARLEDELTELNSPFFKTHVVGSSLLFVNDHGLAKVMWIDGKTVLPDQOM 645  
 QY 121 LSHRLPMAGNRNEDGYL 137  
 DB 646 LSHRLPMAGNRNEDGYL 662  
 RESULT 6  
 ID 07TS72\_MOUSE PRELIMINARY; PRT; 678 AA.  
 AC 07TS72;  
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 13.  
 DE Inositol 1,4,5-trisphosphate 3-kinase C.  
 GN Name=Itpkc;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Heide F.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Tothiyuki S., Carninci P., Mullany S.J.,  
 RA Raba S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J.J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Wilming M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
 RA Scherch A., Schein J.E., Jones S.U.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Limb;  
 RA Strausberg R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
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 CC EMBL; BC053450; AAH53450.1; -, mRNA.  
 DR SNR; 07TS72; 420-678.



DR Ensemble; ENSMUSG0000003752; Mus musculus.  
DR MGI; MGI:2442554; Itpkc.  
DR GO; GO:0008440; F:inositol triphosphate 3-kinase activity; IDA.  
DR InterPro; IPR005522; IPK.  
DR Pfam; PF03770; IPK; 1.  
KW Kinase.  
SQ SEQUENCE 678 AA; 74493 MW; 0D3705B3D682BED CRC64;  
Query Match 90.8%; Score 658; DB 2; Length 678;  
Best Local Similarity 91.2%; Pred. No. 1.4e-53;  
Matches 125; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
QY 1 AVTKRRYQMWRRTMSSTLTGFRIGIKKADGTCNTNFKKTOALBOVTKVLDFVGDGHV 60  
Db 526 AITKRRYQMWRRTLSSTLTGFRIGIKKADGTCNTNFKKTOALBOVTKVLDFVGDGHV 585  
QY 61 ILQKYVACLEBELREALISPPFKTHEVVGSSLLFVHDHTGLAKVMWIDFGKTVALPDHQT 120  
Db 586 ILKRYVARELDRLFTLENSPPFKTHEVVGSSLLFVHDHTGLAKVMWIDFGKTVALPDHQM 645  
QY 121 LSHRLPWAEGNRDEGYL 137  
Db 646 LSHRLPWTENGRDEGYL 662  
RESULT 7  
Q4SPLO\_TERNQ PRELIMINARY; PRT; 300 AA.  
ID Q4SPLO\_TERNQ  
AC Q4SPLO\_TERNQ  
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
DT 19-JUL-2005, sequence version 1.  
DT 07-FEB-2006, entry version 4.  
DE Chromosome 16 SCAPI4537, whole genome shotgun sequence. (Fragment).  
GN ORFNames=STENG0001479001.  
OS Tetradodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetradodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed:15496914; DOI=10.1038/nature03025;  
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,  
RA Maucel E., Bouneau L., Fischer C., Ozouf-Costez C., Bernot A.,  
RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Da Silva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthonard V., Jabin C., Castellani V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Catcolico L., Poulain J., De Bernardis V.,  
RA Crnaud C., Duprat S., Brotier P., Coutanceau J.-P., Gouzy J.,  
RA Parra G., Lardier G., Chappe C., McKernan K.J., McMan P., Boeak S.,  
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Landel V., Schachter V., Quetier F., Saurin W., Scarpetti C.,  
RA Wincker P., Lander B.S., Weissbach J., Roest Crolius H.,  
RT "Genome duplication in the teleost fish Tetradodon nigroviridis reveals  
the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
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CC EMBL; CAE01014537; CAF97422.1; -; Genomic DNA.  
DR SNR; Q4SPLO; 40-295.  
DR GO; GO:0008440; F:inositol triphosphate 3-kinase activity; IEA.  
FT NON\_TER 1 1

SQ SEQUENCE 300 AA; 34775 MW; 5E32D39B508A7EF CRC64;  
Query Match 72.3%; Score 524; DB 2; Length 300;  
Best Local Similarity 72.8%; Pred. No. 3.1e-41;  
Matches 99; Conservative 14; Mismatches 23; Indels 0; Gaps 0;  
QY 2 VTKPRYQMWRRTMSSTLTGFRIGIKKADGTCNTNFKKTOALBOVTKVLDFVGDGHV 61  
Db 147 ILKRYVARELDRLFTLENSPPFKTHEVVGSSLLFVHDHTGLAKVMWIDFGKTVALPDHQT 206  
QY 62 LQKYVACLEBELREALISPPFKTHEVVGSSLLFVHDHTGLAKVMWIDFGKTVALPDHQT 121  
Db 207 LKLYVQRLQIRSVLEQSPFQTHEVVGSSLLFVHDHTGLAKVMWIDFGKTVALPDHQT 266  
QY 122 LSHRLPWAEGNRDEGYL 137  
Db 267 DHRTPWVGNRDEGYL 282  
RESULT 8  
Q5RGF8\_BRARE PRELIMINARY; PRT; 395 AA.  
ID Q5RGF8\_BRARE  
AC Q5RGF8\_BRARE  
DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.  
DT 21-DEC-2004, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE Novel protein similar to vertebrate inositol 1,4,5-trisphosphate 3-  
DE kinase B (ITPKB) (Fragment).  
GN Name=OTTDARPO000006972; ORFNames=CH211-235J18.1-001;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Donaldson S.;  
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Dyer L.;  
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
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CC EMBL; BX649588; CA111856.1; JOINED; Genomic DNA.  
DR EMBL; BX901888; CA111856.1; -; Genomic DNA.  
DR EMBL; BX649588; CA112065.1; -; Genomic DNA.  
DR EMBL; BX901888; CA112065.1; JOINED; Genomic DNA.  
DR SNR; Q5RGF8; 120-389.  
DR Ensemble; ENSDARG0000010059; Danio rerio.  
DR GO; GO:0008440; F:inositol triphosphate 3-kinase activity; IEA.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR InterPro; IPR005522; IPK.  
DR Pfam; PF03770; IPK; 1.  
KW Kinase.  
FT NON\_TER 1 1  
SQ SEQUENCE 395 AA; 45081 MW; 7FDA76067A5D0433 CRC64;  
Query Match 71.3%; Score 517; DB 2; Length 395;  
Best Local Similarity 71.5%; Pred. No. 1.9e-40;  
Matches 98; Conservative 14; Mismatches 25; Indels 0; Gaps 0;  
QY 1 AVTKRRYQMWRRTMSSTLTGFRIGIKKADGTCNTNFKKTOALBOVTKVLDFVGDGHV 60  
Db 240 AVTKRRYQMWRRTLSSTLTGFRIGIKKADGTCNTNFKKTOALBOVTKVLDFVGDGHV 299  
QY 61 ILQKYVACLEBELREALISPPFKTHEVVGSSLLFVHDHTGLAKVMWIDFGKTVALPDHQT 120  
Db 300 ILKRYVARELDRLFTLENSPPFKTHEVVGSSLLFVHDHTGLAKVMWIDFGKTVALPDHQM 359  
QY 121 LSHRLPWAEGNRDEGYL 137



OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
NCBI\_TaxId=8355;  
[1]  
RN NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen.  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.,  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative."  
RL Dev. Dyn. 225:384-391 (2002).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Wozny K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,  
RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[3]  
RN NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen.  
RA Klein S., Gernard D.S.,  
RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NonDerivs license  
CC -----  
DR EMBL; BC110967; AAI10968.1; -; mRNA.  
KW Hypothetical protein.  
SQ SEQUENCE 516 AA; 58271 MW; 2693D817D8AD957A CRC64;  
Query Match 70.8%; Score 513; DB 2; Length 516;  
Best Local Similarity 70.8%; Pred. No. 6.3e-40;  
Matches 97; Conservative 17; Mismatches 23; Indels 0; Gaps 0;  
QY 1 AVTKRYQMRETMSTSLGFRIGIKKADGTCNTNPKTKQALNQYKVLDPDGHV 60  
DB 364 AILKRYQMRETMSTSLGFRIGIKKADGTCNTNPKTKCKEQVIALNPFVDSKN 423  
QY 61 ILQKYVACLEBRLAEISPFKTEHVVGSSLLFVHDHTGLAKVMNIDFGKVALPDHOTL 120  
DB 424 ILRKYLVALKELRLAESEFQSHVVGSSLLFVHDSBQAKVMNIDFGKTRLPDGBEL 483  
QY 121 LSHRLPMAEGNREDEYL 137  
DB 484 LNHRTPWEGNREDEYL 500

DT 19-JUL-2005, sequence version 1.  
DT 07-FEB-2006, entry version 4.  
DE Chromosome 14 SCAP14660, whole genome shotgun sequence. (Fragment).  
GN ORFNames=GSTENG00020685001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorph; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
NCBI\_TaxId=9983;  
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RN NUCLEOTIDE SEQUENCE.  
RX PubMed=15496914; DOI=10.1038/nature03025;  
RA Jallón O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozoul-Costaz C., Bernot A.,  
RA Nicod S., Jaffe D., Fisher S., Luitalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castel V., Katinka M., Vacherie B.,  
RA Biemont C., Skallit Z., Catcolico L., Poulain J., De Bernardis V.,  
RA Chraud C., Duprat S., Brotier P., Coutanceau J.-P., Gouzy J.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan F., Bosak S.,  
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Queller F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype."  
RL Nature 431:946-957 (2004).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC -----  
DR EMBL; CAE01014660; CAG01798.1; -; Genomic DNA.  
DR GO; GO:0008440; F:inositol triphosphate 3-kinase activity; IEA.  
FT NON TER 1 1  
FT NON TER 325 325  
SQ SEQUENCE 325 AA; 37051 MW; DA8AD751AB35AC5 CRC64;  
Query Match 69.9%; Score 507; DB 2; Length 325;  
Best Local Similarity 69.1%; Pred. No. 1.4e-39;  
Matches 94; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
QY 2 VTKRYQMRETMSTSLGFRIGIKKADGTCNTNPKTKQALNQYKVLDPDGHV 61  
DB 177 VTKRYQMRETMSTSLGFRIGIKKADGTCNTNPKTKCKEQVIALNPFVDSKN 236  
QY 62 LQKYVACLEBRLAEISPFKTEHVVGSSLLFVHDHTGLAKVMNIDFGKVALPDHOTL 121  
DB 237 LKCYLSRLERLRLAEISPFKTEHVVGSSLLFVHDSBQAKVMNIDFGKTRLPDGBEL 296  
QY 122 SHRLPMAEGNREDEYL 137  
DB 297 THRKEWEGNREDEYL 312

RESULT 12  
Q4SC34\_TETNG PRELIMINARY; PRT; 325 AA.  
AC Q4SC34;  
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.

RESULT 13  
Q4RM63\_TETNG PRELIMINARY; PRT; 425 AA.  
AC Q4RM63;  
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
DT 19-JUL-2005, sequence version 1.  
DT 07-FEB-2006, entry version 4.  
DE Chromosome 10 SCAP15019, whole genome shotgun sequence. (Fragment).  
GN ORFNames=GSTENG00032195001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorph; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN  
RP NOCLEOTIDE SEQUENCE.  
RX PubMed:15496914; DOI=10.1038/nature03025;  
RA Jallien O., Aury J.-M., Brunet P., Petit J.-L., Strange-Thomann N.,  
RA Micaud E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Desliva C., Salenoudat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jabin C., Castellani V., Kacinka M., Vacherie B.,  
RA Blemont C., Skalli Z., Cattellico L., Poullain J., De Berardinis V.,  
RA Cnaud C., Duprat S., Broctier P., Coutanceau J.-P., Gouzy J.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Wolf J.-N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Landel V., Schachter V., Queller F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN  
RP NOCLEOTIDE SEQUENCE.  
RG Genoscope, Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC  
DR EMBL: CAE01015019; CAG10519.1; -; Genomic DNA.  
DR GO: GO:0008440; F:inositol triphosphate 3-kinase activity; IEA.  
FT NON\_TER 425  
SQ SEQUENCE 425 AA; 47839 MW; 001F0AA21514030E CRC64;  
Query March 69.8%; Score 506; DB 2; Length 425;  
Best Local Similarity 66.9%; Pred. No. 2.3e-39;  
Matches 91; Conservative 23; Mismatches 22; Indels 0; Gaps 0;  
QY 2 VTKERYMOWRETNSTSTLTGFRIGIKKADGTCNTNPFKKTQALQVTVLEDFVYGDHVI 61  
DB 275 VTKERYMOWRETNSTSTLTGFRIGIKKADGTCNTNPFKKTQALQVTVLEDFVYGDHVI 334  
QY 62 LQKTVACLEERALEISPPFKTHEVVGSSLLFVHDHTGLAKVMWIDFGKVALPDHOTL 121  
DB 335 IKSYLSRLREIQRALKKSAFFKQHEVIGSSLLFHDHTGKQVWIDFGKTTALPEGQTL 394  
QY 122 SHRLPWAEGNRDEGYL 137  
DB 395 KHDVPMQEGNRDEGYL 410  
RESULT 14  
IP3KA MOUSE STANDARD: PRT; 459 AA.  
AC Q8R071; Integrated into UniProtKB/Swiss-Prot.  
DT 19-JUN-2004, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-2002, sequence version 1.  
DT 07-FEB-2006, entry version 18.  
DE Inositol-tri-phosphate 3-kinase A (EC 2.7.1.127) (Inositol 1,4,5-  
DE triphosphate 3-kinase A) (IP3K A) (IP3 3-kinase A).  
GN Name:ItpkA;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NOCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC STRAIN=FVB/N; TISSUE=Mammary tumor;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Cantinici P., Prange C.,  
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Motley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhe U.E.,  
RA Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- CATALYTIC ACTIVITY. ATP + 1D-myo-inositol 1,4,5-trisphosphate =  
CC ADP + 1D-myo-inositol 1,3,4,5-tetrakisphosphate.  
CC -1- ENZYME REGULATION. IP3K is activated by calmodulin (By  
CC similarity).  
CC -1- SIMILARITY: Belongs to the inositol phosphokinase (IPK) family.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs license  
CC  
DR EMBL: BC027291; AAH27291.1; -; mRNA.  
DR SMR: Q8R071; 185-459.  
DR InFect: Q8R071; -;  
DR Ensembl: ENSMUSG0000027296; Mus musculus.  
DR MGI: MGI:1333822; ItpkA.  
DR GO: GO:0004428; F:inositol or phosphatidylinositol kinase act. .; TAS.  
DR GO: GO:0006020; P:myo-inositol metabolism; IMP.  
DR InterPro: IPR005522; IPK.  
DR Pfam: PF03770; IPK; 1.  
DR ATP-binding; Calmodulin-binding; Kinase; Nucleotide-binding;  
KM Transferrase.  
FT CHAIN 1 459 Inositol-tri-phosphate 3-kinase A.  
FT NP\_BIND 247 249 /FTID=PRO\_000006866.  
FT REGION 285 293 Calmodulin-binding (By similarity).  
FT BINDING 310 317 Substrate binding (By similarity).  
FT BINDING 195 195 ATP (By similarity).  
FT BINDING 207 207 ATP (By similarity).  
FT BINDING 260 260 ATP (By similarity).  
FT BINDING 262 262 Substrate (By similarity).  
FT BINDING 283 283 Substrate (By similarity).  
FT BINDING 334 334 ATP (By similarity).  
FT BINDING 414 414 ATP (By similarity).  
FT BINDING 417 417 Substrate (By similarity).  
SQ SEQUENCE 459 AA; 50935 MW; 3CDA79DD267A1A5D CRC64;  
Query March 69.8%; Score 506; DB 1; Length 459;  
Best Local Similarity 67.2%; Pred. No. 2.5e-39;  
Matches 92; Conservative 22; Mismatches 23; Indels 0; Gaps 0;  
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DB 367 VLRRYVLRQLQRIITLISDFFRHEVIGSSLLFVHDHTGKQVWIDFGKTTALPEGQTL 426  
QY 121 LSHRLPWAEGNRDEGYL 137  
DB 427 LDHRRPWAEGNRDEGYL 443

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 ID IP3KA RAT STANDARD; PRT; 459 AA.  
 AC P17105;  
 DT 01-AUG-1990, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1991, sequence version 3.  
 DE 07-FEB-2006, entry version 42.  
 DE Inositol-trisphosphate 3-kinase A (EC 2.7.1.127) (inositol 1,4,5-  
 DE trisphosphate 3-kinase A) (IP3K A) (IP3 3-kinase A).  
 GN Name=Itcpka;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Rattus.  
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 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RX MEDLINE=91090700; PubMed=2176078;  
 RA Takazawa K., Vandekerckhove J., Dumont J.E., Erneux C.;  
 RT "Cloning and expression in Escherichia coli of a rat brain cDNA  
 RT encoding a Ca<sup>2+</sup>/calmodulin-sensitive inositol 1,4,5-trisphosphate 3-  
 RT kinase.";  
 RL Biochem. J. 272:107-112(1990).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=90208336; PubMed=2157285;  
 RA Choi K.Y., Kim H.K., Lee S.Y., Moon K.H., Sim S.S., Kim J.W.,  
 RA Chung H.K., Rhee S.G.;  
 RT "Molecular cloning and expression of a complementary DNA for inositol  
 RT 1,4,5-trisphosphate 3-kinase.";  
 RL Science 248:64-66(1990).  
 RN [3]  
 RP PROTEIN SEQUENCE OF 315-326, AND ACTIVE SITE.  
 RX MEDLINE=95374430; PubMed=7646431;  
 RA Communi D., Lecocq R., Vanweyenbergh V., Erneux C.;  
 RT "Active site labelling of inositol 1,4,5-trisphosphate 3-kinase A by  
 RT phenylglyoxal.";  
 RL Biochem. J. 310:109-115(1995).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 185-459 IN COMPLEX WITH ADP.  
 RX PubMed=15350215; DOI=10.1016/j.molcel.2004.08.005;  
 RA Miller G.J., Hurley J.H.;  
 RT "Crystal structure of the catalytic core of inositol 1,4,5-  
 RT trisphosphate 3-kinase.";  
 RL Mol. Cell 15:703-711(2004).  
 CC -1- CATALYTIC ACTIVITY: ATP + 1D-myo-inositol 1,4,5-trisphosphate =  
 CC ADP + 1D-myo-inositol 1,3,4,5-tetrakisphosphate.  
 CC -1- ENZYME REGULATION: IP3K is activated by calmodulin.  
 CC -1- SIMILARITY: Belongs to the inositol phosphokinase (IPK) family.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonCommercial  
 CC License  
 CC EMBL; X56917; CA440248.1; -, mRNA.  
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 DR RGD; 619950; Itcpka.  
 DR GO; GO:0004665; F:calcium- and calmodulin-dependent protein k. . .; IDA.  
 DR GO; GO:0008440; F:inositol trisphosphate 3-kinase activity; IDA.  
 DR InterPro; IPRO05522; IPK.  
 DR Pfam; PF03770; IPK; 1.  
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 FT REGION 310 317  
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 FT Calmodulin-binding.  
 FT Substrate binding (By similarity).  
 FT ATP (By similarity).  
 FT ATP.

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Query Match 69.8%; Score 506; DB 1; Length 459;  
 Best Local Similarity 67.2%; Pred. No. 2.5e-39;  
 Matches 92; Conservative 22; Mismatches 23; Indels 0; Gaps 0;

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Db	367	VLRKYLNRLOQIRITLTISDFPRHREVISSLLFVHDHCRAGVWLIDFGKTTLPDGOI	426
Qy	121	LSHRLPMAEGNRREDGYL	137
Db	427	LDHRRPMEEGNRREDGYL	443

Mon May 22 09:43:34 2006

us-10-781-581-226.rup

Page 10

Search completed: May 21, 2006, 04:25:26  
Job time : 299 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 21, 2006, 04:25:44 ; Search time 50 Seconds  
(without alignments)  
239.834 Million cell updates/sec

Title: US-10-781-581-226  
Perfect score: 725

Sequence: 1 AVTKPRYMQRRTMSSTSL.....HQTLSHRLPWAEGNREDGYL 137

Scoring table: BLOSUM62

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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**Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	504	69.5	464	2	US-09-949-016-10505
2	493	68.0	472	2	US-09-949-016-6194
3	493	68.0	504	2	US-09-949-016-8219
4	403.5	55.7	397	2	US-09-270-767-33291
5	403.5	55.7	397	2	US-09-270-767-48508
6	74.5	10.3	390	2	US-09-107-532A-6615
7	72.5	10.0	817	2	US-09-543-681A-4637
8	71	9.8	2141	2	US-09-949-016-10918
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10	70	9.7	645	2	US-09-315-127-8
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13	70	9.7	654	2	US-09-315-127-12
14	69.5	9.6	833	1	US-08-844-086-2
15	69.5	9.6	833	2	US-09-018-211-2
16	69	9.5	260	2	US-09-328-352-6563
17	69	9.5	293	2	US-10-094-749-2660
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22	69	9.5	1312	2	US-09-554-572-26
23	68	9.4	248	2	US-09-610-185C-2
24	68	9.4	249	2	US-09-610-185C-4
25	68	9.4	580	2	US-10-104-047-3215
26	68	9.4	978	2	US-09-949-016-8098

27	68	9.4	1136	2	US-09-275-2822A-9	Sequence 9, Appli
28	68	9.4	1236	2	US-09-176-664-21	Sequence 21, Appli
29	68	9.4	1236	2	US-09-519-076-21	Sequence 21, Appli
30	68	9.4	2486	2	US-09-123-028-2	Sequence 2, Appli
31	68	9.4	2958	2	US-08-894-344C-2	Sequence 2, Appli
32	68	9.4	2958	2	US-09-678-023A-2	Sequence 2, Appli
33	67.5	9.3	219	2	US-08-924-747-4	Sequence 4, Appli
34	67.5	9.3	219	2	US-09-247-373B-4	Sequence 4, Appli
35	67.5	9.3	219	2	US-09-296-715-4	Sequence 4, Appli
36	67.5	9.3	631	2	US-09-944-016-10729	Sequence 10729, A
37	67	9.2	620	2	US-09-328-352-7730	Sequence 7730, Appl
38	67	9.2	888	2	US-09-583-110-3750	Sequence 3750, Appl
39	67	9.2	889	2	US-09-107-433-3196	Sequence 3196, Appl
40	67	9.2	917	2	US-09-976-594-709	Sequence 709, App
41	67	9.2	917	2	US-09-919-039-775	Sequence 275, Appli
42	67	9.2	946	2	US-09-074-579-3	Sequence 3, Appli
43	67	9.2	946	2	US-09-388-774-3	Sequence 3, Appli
44	67	9.2	946	2	US-09-546-153-1	Sequence 1, Appli
45	67	9.2	964	2	US-09-544-016-10806	Sequence 10806, A

## ALIGNMENTS

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US-09-949-016-10505
; Sequence 10505, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10505
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10505

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QY      121 LSHRLPWAEGNRDEGYL 137
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DB      432 LDHRRPWEGRNDEGYL 448
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RESULT 2
US-09-949-016-6194
; Sequence 6194, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

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: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
:
: FILE REFERENCE: CLO01107
:
: CURRENT APPLICATION NUMBER: US/09/949,016
:
: CURRENT FILING DATE: 2000-04-14
:
: PRIOR APPLICATION NUMBER: 60/241,755
:
: PRIOR FILING DATE: 2000-10-20
:
: PRIOR APPLICATION NUMBER: 60/237,768
:
: PRIOR FILING DATE: 2000-10-03
:
: PRIOR APPLICATION NUMBER: 60/231,498
:
: PRIOR FILING DATE: 2000-09-08
:
: NUMBER OF SEQ ID NOS: 207012
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 6194
:
: LENGTH: 472
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: TYPE: prt
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: ORGANISM: Human
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: US-09-949-016-6194

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Best Local Similarity	67.9%	Pred	No	1.7e-50;					
Matches	93,	Conservative	14,	Mismatches	30,	Indels	0;	Gaps	0

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Db 316 AVTKPRYMOMRETTSTLGRISGIKKEDGVNDDPFKTKREOVTELEFREFTYGNHN 375
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Qy 61 ILQKVVACIEELREALIEISPPFKTHVVGSSLLFVHDHTGLAKVMNIDFGKTALPDHOT 120
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Db 376 ILIARDRIKARITTELEVSPPFKCHEVITGSSLLFIHDKKEQAKVMNIDFGKTPLPDGGOT 435
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Qy 121 LSHRLPMAEGNREDGYL 137
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RESULT 3
US-09-949-016-8219
; Sequence 8219, Application US/09949016
; Patent No. 6812359
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
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US-09-949-016-8219

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Db 468 LQHDVPMQEGNREDDYL 484

RESULT 4  
US-09-270-767-33291  
; Sequence 33291, Application US/09270767

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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OR INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33291
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33291

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Db 271 ILPRITQRRARATLAVSEFPQTEHVIGSSLLFVHDHT-ASIMLIDPAKTVLEPPQLR 329
QY 121 LSHRLPMAEGNREDGYL 137
Db 330 IDHYSAMKVGNNHEDGYL 346

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RESULT 5
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; Sequence 48508, Application US/09270767
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; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: prt
; ORGANISM: Drosophila melanogaster
US-09-270-767-48508

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QY 1 AATKRRYQWMBRTSTSTSLFRIGIKKADGTCNNFEKQTALBOVTALBEDFYVGDH 60  
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 QY 61 ILQKVVACLEELREALETSPEFKTEHVYSSLLFYVDHTGLAKWMMIDFGKVALPDHOT 120  
 DB 271 ILPRYIQRRARATLAVSEFFQTEHVYSSLLFYVDHT-ASIWLDFAKTVELPQLR 329  
 QY 121 LSHRLPMALGNREDGYL 137  
 DB 330 IDHYSAMKVGNNHEDGYL 346



RESULT 6  
US-09-107-532A-6615  
; Sequence 6615, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 6615:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 390 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...390  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6615:  
US-09-107-532A-6615  
Query Match 10.3%; Score 74.5; DB 2; Length 390;  
Best Local Similarity 29.7%; Pred. No. 2.9;  
Matches 33; Conservative 10; Mismatches 31; Indels 37; Gaps 5;  
QY 37 NFKKQALBOVTK-----VLDFVDGDHVIILQKVVACCELRLEALISPFKTH 85  
DB 190 DFLKSEVLENDYTKKVALTEBQEQALSLFKTDVNVHKYDDMLILKLTGLRLS----- 243  
QY 86 EVVGSLLFVHDHTGLAKVMIDFGKTVAPDHQTLSHRLPWAEGNREDGY 136  
DB 244 ELGCG---LTVAD-----IDFKNEVLIIDHQLK-----NKGQY 274  
RESULT 7  
US-09-543-681A-4637  
; Sequence 4637, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709,1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 4637  
; LENGTH: 817  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-4637  
Query Match 10.0%; Score 72.5; DB 2; Length 817;  
Best Local Similarity 25.2%; Pred. No. 15;  
Matches 28; Conservative 21; Mismatches 31; Indels 31; Gaps 5;  
QY 40 KTOALBOVTKVLEDFVDGDHVIILQKVV-----ACLEEL--REALISPFK 83  
DB 260 KTDALNGVKVYIKH-----DVLANKYITGINKSGQGEVYSLVEQLNDKESITISQYND 315  
QY 84 THEVGSLLFVHDHTGLAKVMIDFGKTVAPDHQTLSHRLPWAEGNRED 134  
DB 316 IRAFFGISAFHLSONIGVSATFLANFAKTHAL-----TISK-----NKQD 355  
RESULT 8  
US-09-949-016-10918  
; Sequence 10918, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10918  
; LENGTH: 2141  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10918  
Query Match 9.8%; Score 71; DB 2; Length 2141;  
Best Local Similarity 21.6%; Pred. No. 88;  
Matches 35; Conservative 20; Mismatches 53; Indels 54; Gaps 5;  
QY 8 MOWRET-----MSTSTLGRLEGTKKADGTNTNF-----KKTQ 42  
DB 1920 LSWNESTIRIETOERPRDVSVELMKYHGINAIEFTSKNFSACLBIKESILORHQ 1979  
QY 43 ALBOVTKVLEDFVDGDHVIILQKVVACCELRLEALISPFKTHEVGSLLFVHDHTGLA 102  
DB 1980 ASEIEIKKQVWRSRKNEMKEKFAERERKMLLEVCOFSRDSV-----A 2025  
QY 103 KVMNI-----DFKTVAPDHQTLSHR-----LPWAE 129  
DB 2026 EAWLIAQEPYLASGDFGHTVDSVEKLKHEAFKSTASWAE 2067  
RESULT 9  
US-10-104-047-3353  
; Sequence 3353, Application US/10104047  
; Patent No. 6943241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE

```

; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3353
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-3353

Query Match
Best Local Similarity 36.1%; Score 70; DB 2; Length 274;
Matches 22; Conservative 11; Mismatches 20; Indels 8; Gaps 2;

QY 23 RIEG---IKKADGTCTNFKKTOALEQVTKLEDFVGDHVLIOKKVACLEELREALEI 78
DB 74 RIEGKDEIRRADLCRIKMEKLEBEENLTRELKSEIER---LQKRMALFKLEAFSR 129

QY 79 S 79
DB 130 S 130

RESULT 10
US-09-315-127-8
; Sequence 8, Application US/09315127
; Patent No. 6448390
; GENERAL INFORMATION:
; APPLICANT: The University of Tennessee, c/o Richard Cox
; TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
; FILE REFERENCE: 44137-5023, U. of Tennessee
; CURRENT APPLICATION NUMBER: US/09/315,127
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-315-127-8

Query Match
Best Local Similarity 29.2%; Score 70; DB 2; Length 645;
Matches 31; Conservative 15; Mismatches 46; Indels 14; Gaps 5;

QY 11 RETMSSTLT---GFRIGIKKADGTCTNFKKTOALEQVTKLE---DFVGDHVLIOK 64
DB 449 REPVSLTALLLGGITWGGIAGIGTGTALTALIKTQDFQLHAAIQTDLNEVEKSTINLEK 508

QY 65 YVACLEEL---REALISPFKTHEVGS---SLFVHDHTGLAK 103
DB 509 SLTSLSEVVLQNRRLDIL-FLKEGGLCAALKECCFYADHTGLVR 553

RESULT 11
US-09-315-127-9
; Sequence 9, Application US/09315127
; Patent No. 6448390
; GENERAL INFORMATION:
; APPLICANT: The University of Tennessee, c/o Richard Cox
; TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
; FILE REFERENCE: 44137-5023, U. of Tennessee
; CURRENT APPLICATION NUMBER: US/09/315,127
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-315-127-9
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; LENGTH: 645
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SEQ. ID NO.
; OTHER INFORMATION: 6, envelope protein produced by retroviral vector
; OTHER INFORMATION: of seq. id no. 5
; US-09-315-127-9

Query Match
Best Local Similarity 29.2%; Score 70; DB 2; Length 645;
Matches 31; Conservative 15; Mismatches 46; Indels 14; Gaps 5;

QY 11 RETMSSTLT---GFRIGIKKADGTCTNFKKTOALEQVTKLE---DFVGDHVLIOK 64
DB 449 REPVSLTALLLGGITWGGIAGIGTGTALTALIKTQDFQLHAAIQTDLNEVEKSTINLEK 508

QY 65 YVACLEEL---REALISPFKTHEVGS---SLFVHDHTGLAK 103
DB 509 SLTSLSEVVLQNRRLDIL-FLKEGGLCAALKECCFYADHTGLVR 553

RESULT 12
US-09-315-127-11
; Sequence 11, Application US/09315127
; Patent No. 6448390
; GENERAL INFORMATION:
; APPLICANT: The University of Tennessee, c/o Richard Cox
; TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
; FILE REFERENCE: 44137-5023, U. of Tennessee
; CURRENT APPLICATION NUMBER: US/09/315,127
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-315-127-11

Query Match
Best Local Similarity 29.2%; Score 70; DB 2; Length 654;
Matches 31; Conservative 15; Mismatches 46; Indels 14; Gaps 5;

QY 11 RETMSSTLT---GFRIGIKKADGTCTNFKKTOALEQVTKLE---DFVGDHVLIOK 64
DB 458 REPVSLTALLLGGITWGGIAGIGTGTALTALIKTQDFQLHAAIQTDLNEVEKSTINLEK 517

QY 65 YVACLEEL---REALISPFKTHEVGS---SLFVHDHTGLAK 103
DB 518 SLTSLSEVVLQNRRLDIL-FLKEGGLCAALKECCFYADHTGLVR 562

RESULT 13
US-09-315-127-12
; Sequence 12, Application US/09315127
; Patent No. 6448390
; GENERAL INFORMATION:
; APPLICANT: The University of Tennessee, c/o Richard Cox
; TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
; FILE REFERENCE: 44137-5023, U. of Tennessee
; CURRENT APPLICATION NUMBER: US/09/315,127
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: SEQ. ID NO.
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OTHER INFORMATION: 8, envelope protein produced by retroviral vector  
OTHER INFORMATION: of seq. id no. 7  
US-09-315-127-12

Query Match 9.7%; Score 70; DB 2; Length 654;  
Best Local Similarity 29.2%; Pred. No. 21;  
Matches 31; Conservative 15; Mismatches 46; Indels 14; Gaps 5;

QY 11 RETMSTSTL--GPRIGIKKADGTCNTNFKKTOALBOVTYVLE---DFVGDHVILOK 64  
DB 458 REPVSLLTALLGTLGTMGIALGIGTALIKTQOPELHAIQTDLNEVKSITNLEK 517  
QY 65 YVACLEEL---REALISPFKTHVWGS---SLFVHDHTGLAK 103  
DB 518 SLTSLSEVVLQNRRLGDL-LFKEGGLCALKECCFYADHTGLVR 562

RESULT 14  
US-08-844-086-2  
Sequence 2, Application US/08844086  
Patent No. 5866390

GENERAL INFORMATION:  
APPLICANT: Lawlor, Elizabeth  
TITLE OF INVENTION: No. 5866390e1 Compounds  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA

COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/844,086  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9607993.4  
FILING DATE: 18-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimm, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P31457-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 833 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-844-086-2

Query Match 9.6%; Score 69.5; DB 1; Length 833;  
Best Local Similarity 23.7%; Pred. No. 34;  
Matches 31; Conservative 13; Mismatches 40; Indels 47; Gaps 6;

QY 37 NFKKTQALEQVTKYLEDVFG--DHVILQKYVACLE-----LREALISPFK 83  
DB 366 NVEBAAYTEDEGLHVNDFLDGLNKEDAIKIVACLEEGCGQEKVYRLRWL-----FS 420  
QY 84 THEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPD-----HOTLSHR 124  
DB 421 RQRWGEPIPIH-----W--EDGTSTAVPETELPVLVPTKDIRPSGTGSSPLANTL 470

QY 125 LPWAEGRNEDG 135  
DB 471 TDWLEVTREDDG 481

RESULT 15  
US-09-018-211-2  
Sequence 2, Application US/09018211  
Patent No. 6048716

GENERAL INFORMATION:  
APPLICANT: Lawlor, Elizabeth  
TITLE OF INVENTION: No. 6048716e1 Compounds  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA

COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/018,211  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/844,086  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: 9607993.4  
FILING DATE: 18-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimm, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P31457-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 833 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-018-211-2

Query Match 9.6%; Score 69.5; DB 2; Length 833;  
Best Local Similarity 23.7%; Pred. No. 34;  
Matches 31; Conservative 13; Mismatches 40; Indels 47; Gaps 6;

QY 37 NFKKTQALEQVTKYLEDVFG--DHVILQKYVACLE-----LREALISPFK 83  
DB 366 NVEBAAYTEDEGLHVNDFLDGLNKEDAIKIVACLEEGCGQEKVYRLRWL-----FS 420  
QY 84 THEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPD-----HOTLSHR 124  
DB 421 RQRWGEPIPIH-----W--EDGTSTAVPETELPVLVPTKDIRPSGTGSSPLANTL 470  
QY 125 LPWAEGRNEDG 135  
DB 471 TDWLEVTREDDG 481

Search completed: May 21, 2006, 04:27:04  
Job time : 51 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OW protein - protein search, using sw model

Run on: May 21, 2006, 04:26:24 ; Search time 176 Seconds  
(without alignments)  
360.571 Million cell updates/sec

Title: US-10-781-581-226

Perfect score: 725

Sequence: 1 AVTKPRYQMQRMTSSTL.....HQTLSRLPMAEGNRDEGYL 137

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

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2: /EMC\_Celestra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celestra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celestra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
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6: /EMC\_Celestra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	725	100.0	137	US-10-781-581-226	Sequence 226, App
2	725	100.0	660	US-10-311-034-26	Sequence 26, Appl
3	725	100.0	683	US-10-092-900A-342	Sequence 342, App
4	493	68.0	798	US-10-168-582-5	Sequence 5, Appli
5	493	68.0	798	US-10-979-095-5	Sequence 1, Appli
6	482	66.5	1192	US-10-764-330-1	Sequence 182, App
7	464	64.0	1339	US-10-082-830-282	Sequence 175, Ap
8	403.5	55.7	316	US-10-042-894A-25	Sequence 25, Appl
9	382.5	52.8	71	US-10-029-366-29832	Sequence 25, Appl
10	145	20.0	325	US-10-408-765A-1520	Sequence 1520, Ap
11	81.5	11.2	349	US-10-369-493-175	Sequence 175, App
12	80.5	11.1	248	US-11-096-568A-32990	Sequence 32990, A
13	79.5	11.0	300	US-11-096-568A-32989	Sequence 32989, A
14	79.5	11.0	300	US-11-096-568A-32988	Sequence 32988, A
15	79.5	11.0	300	US-11-188-298-12964	Sequence 12964, A
16	79	10.9	422	US-10-042-894A-10	Sequence 10, Appl
17	78	10.8	279	US-10-424-599-249309	Sequence 249309,
18	78	10.8	279	US-10-506-454-333	Sequence 333, App
19	76	10.6	496	US-10-767-701-43815	Sequence 43815, A
20	75.5	10.4	392	US-10-437-963-202651	Sequence 202651,
21	75.5	10.4	977	US-10-425-114-51119	Sequence 51119, A
22	75.5	10.3	317	US-10-425-114-42633	Sequence 42633, A
23	75	10.3	455	US-11-096-568A-24584	Sequence 24584, A
24	74	10.2	417	US-10-437-963-203451	Sequence 203451,
25	74	10.2	417	US-11-096-568A-24583	Sequence 24583, A
26	74	10.2	417	US-11-096-568A-24583	Sequence 24583, A
27	74	10.2	417	US-11-096-568A-24583	Sequence 24583, A

28	74	10.2	455	6	US-11-096-568A-24582	Sequence 24582, A
29	74	10.2	561	4	US-10-437-963-172520	Sequence 172520, A
30	73.5	10.1	602	4	US-10-156-761-10462	Sequence 10462, A
31	73.5	10.1	634	5	US-10-739-930-6363	Sequence 6363, Ap
32	73	10.1	1371	4	US-10-437-963-183969	Sequence 183969,
33	72.5	10.0	240	4	US-10-283-122A-71183	Sequence 71183, A
34	72.5	10.0	362	4	US-10-283-122A-63450	Sequence 63450, A
35	72.5	10.0	767	6	US-11-079-463-8192	Sequence 8192, Ap
36	72	9.9	397	4	US-10-437-963-112279	Sequence 112279,
37	72	9.9	410	4	US-10-415-011-15	Sequence 15, Appl
38	72	9.9	467	4	US-10-362-774-3	Sequence 6071, Ap
39	72	9.9	467	4	US-10-362-774-3	Sequence 6071, Ap
40	72	9.9	606	4	US-10-156-761-13742	Sequence 13742, A
41	72	9.9	1325	4	US-10-437-963-182507	Sequence 182507,
42	71.5	9.9	636	4	US-10-389-586-1296	Sequence 1296, Ap
43	71.5	9.9	636	5	US-10-732-923-9642	Sequence 9642, Ap
44	71.5	9.9	2106	4	US-10-408-765A-2093	Sequence 2093, Ap
45	71	9.8	215	4	US-10-425-114-39157	Sequence 39157, A

## ALIGNMENTS

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RESULT 1
US-10-781-581-226
; Sequence 226, Application US/10781581
; Publication No. US20050019746A1
; GENERAL INFORMATION:
; APPLICANT: Birk Therapeutics Ltd.
; APPLICANT: Seery, Liam
; APPLICANT: Hayes, Ian
; APPLICANT: Murphy, Finbar
; TITLE OF INVENTION: Apoptosis-Related Kinase/GPCRs
; FILE REFERENCE: 8912/2015
; CURRENT APPLICATION NUMBER: US/10/781,581
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 10/764,238
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/457,533
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: UK 0301566.6
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 226
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-581-226

Query Match      100.0%; Score 725; DB 5; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.1e-73;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTKPRYQMQRMTSSTLGFRIEIKKAGTCNTNKTKQALBOVKVLEDFVGDHV 60
DB 1 AVTKPRYQMQRMTSSTLGFRIEIKKAGTCNTNKTKQALBOVKVLEDFVGDHV 60
QY 61 ILQKVVACLEIRLEALBISPFKTHEVVGSILFVHDHTGLAKVWMDFGKTVALLPDHOT 120
DB 61 ILQKVVACLEIRLEALBISPFKTHEVVGSILFVHDHTGLAKVWMDFGKTVALLPDHOT 120
QY 121 LSHRLPMAEGNRDEGYL 137
DB 121 LSHRLPMAEGNRDEGYL 137

RESULT 2
US-10-311-034-26
; Sequence 26, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
```

APPLICANT: YUE, Henry  
APPLICANT: LAL, Preeti  
APPLICANT: BANDMAN, Olga  
APPLICANT: BOROMSKY, Mark L.  
APPLICANT: AU-YOUNG, Janice  
APPLICANT: LU, Yan  
APPLICANT: GANDHI, Ameena R.  
APPLICANT: TRIBOULEY, Catherine M.  
APPLICANT: CHAWLA, Narinder K.  
APPLICANT: YAO, Monique G.  
APPLICANT: LU, Dzung Anna M.  
APPLICANT: GREENWALD, Sara R.  
APPLICANT: RAMKUMAR, Jayalaxmi  
APPLICANT: GRIFFIN, Jennifer A.  
APPLICANT: KEARNEY, Liam  
APPLICANT: BURFORD, Neil  
APPLICANT: NGUYEN, Daniel B.  
APPLICANT: TANG, Y. Tom  
APPLICANT: BAUGHN, Mariah R.  
APPLICANT: HE, Ann  
APPLICANT: THORNTON, Michael  
APPLICANT: HARALIA, April  
APPLICANT: ARVIZU, Chandra S.  
APPLICANT: GURURAJAN, Rajagopal  
APPLICANT: LO, Terence P.  
APPLICANT: KHAH, Farrah A.  
APPLICANT: RECIPON, Shirley A.  
APPLICANT: AZIMZAI, Yalda  
APPLICANT: POLICKY, Jennifer L.  
APPLICANT: DING, Li  
APPLICANT: GREYER, Megan  
APPLICANT: ELIOTT, Vicki S.  
APPLICANT: THANGAVELU, Kavitha  
APPLICANT: BATRA, Sajeew  
APPLICANT: ISON, Craig H.  
TITLE OF INVENTION: HUMAN KINASES  
FILE REFERENCE: PI-0125 PCT  
CURRENT APPLICATION NUMBER: US/10/311.034  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;  
60/228,056  
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: PERL Program  
SEQ ID NO 26  
LENGTH: 660  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040023242A1 7480774CD1  
US-10-311-034-26

Query Match 100.0%; Score 725; DB 4; Length 660;  
Best Local Similarity 100.0%; Pred. No. 3.2e-72;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTKPRYQWQREMTSSTLTGFRLEGIKKADGTCNTNFKTKQALQVTKVLEDPVDDGHV 60  
DB 508 AVTKPRYQWQREMTSSTLTGFRLEGIKKADGTCNTNFKTKQALQVTKVLEDPVDDGHV 567  
QY 61 ILQKYVACLIELREALISPPFKTHEVVGSSLLFVHDHTGLAKVMIDFGKTVALLPDHQT 120  
DB 568 ILQKYVACLIELREALISPPFKTHEVVGSSLLFVHDHTGLAKVMIDFGKTVALLPDHQT 627  
QY 121 LSHRLPWAEGNRDEGYL 137  
DB 628 LSHRLPWAEGNRDEGYL 644

RESULT 3  
US-10-092-900A-342

Sequence 342, Application US/10092900A  
Publication No. US20040043382A1  
GENERAL INFORMATION:  
APPLICANT: Padigar, Murajidhara  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Taupler Jr., Raymond J.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Li, Li  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Gusev, Vladimyr Y.  
APPLICANT: Ji, Weizhen  
APPLICANT: Gorman, Linda  
APPLICANT: Miller, Charles E.  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Patturajan, Meera  
APPLICANT: Gangoli, Beha A.  
APPLICANT: Vernet, Corine A.M.  
APPLICANT: Guo, Xiaojia Saeha  
APPLICANT: Tchernev, Velizar T.  
APPLICANT: Fernandes, Elma R.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Liu, Yi  
APPLICANT: Anderson, David W.  
APPLICANT: Spaderna, Steven K.  
APPLICANT: Catterton, Elina  
APPLICANT: Lette, Mario W.  
APPLICANT: Zhong, Hailong  
APPLICANT: Alsobrook, John P.  
APPLICANT: Lepley, Denise M.  
APPLICANT: Rieger, Daniel K.  
APPLICANT: Burgess, Catherine E.  
TITLE OF INVENTION: No. US20040043382A1 Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-290C  
CURRENT APPLICATION NUMBER: US/10/092.900A  
CURRENT FILING DATE: 2002-03-07  
PRIOR APPLICATION NUMBER: USSN 60/274,322  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USSN 60/283,675  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: USSN 60/338,092  
PRIOR FILING DATE: 2001-12-03  
PRIOR APPLICATION NUMBER: USSN 60/274,281  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USSN 60/274,191  
PRIOR FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: USSN 60/325,681  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: USSN 60/304,354  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: USSN 60/279,995  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: USSN 60/294,899  
PRIOR FILING DATE: 2001-05-31  
PRIOR APPLICATION NUMBER: USSN 60/287,424  
PRIOR FILING DATE: 2001-04-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 768  
SEQ ID NO 342  
LENGTH: 683  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-092-900A-342

Query Match 100.0%; Score 725; DB 4; Length 683;  
Best Local Similarity 100.0%; Pred. No. 3.4e-72;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTKPRYQWQREMTSSTLTGFRLEGIKKADGTCNTNFKTKQALQVTKVLEDPVDDGHV 60  
DB 531 AVTKPRYQWQREMTSSTLTGFRLEGIKKADGTCNTNFKTKQALQVTKVLEDPVDDGHV 590



Db 929 ILIAYRRLKAIKATLRLISPFKCHEVIGSSLLFTHDKKEQAKVMMIDFGKTTPLPREGQT 988  
Qy 121 LSHRLPWAEGNREGDYL 137  
Db 989 LQHDVPWQEGNREGDYL 1005

RESULT 7  
US-10-082-830-282

; Sequence 282, Application US/10082830  
; Publication No. US20030077604A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Yongsang  
; APPLICANT: Recipon, Heeye  
; APPLICANT: Salceda, Susana  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Turner, Leah  
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific  
; FILE REFERENCE: DEX-0249  
; CURRENT APPLICATION NUMBER: US/10/082,830  
; CURRENT FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 60/243,802  
; PRIOR FILING DATE: 2000-10-27  
; NUMBER OF SEQ ID NOS: 282  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 282  
; LENGTH: 1339  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-082-830-282

Query Match 64.0%; Score 464; DB 4; Length 1339;  
Best Local Similarity 53.1%; Pred. No. 1,8e-42;  
Matches 93; Conservative 14; Mismatches 30; Indels 38; Gaps 1;

Qy 1 AVTKRYMQRMTWSSTLTGFRIGIK----- 28  
Db 1145 AVTKRYMQRMTWSSTLTGFRIGIKLRSGAMGALPTARSGNRLHPGLLPQOVLV 1204  
Qy 29 -----KADGCTNPFKKTQALEQVTKVLEDFVDDHYILQKYVACLEALREALEISPF 82  
Db 1205 LSKATKEDGTVNDRPFKTKREQVTEAFREFTKGNHILLAYDRLLKAITTLEVSPPF 1264  
Qy 83 KTHVVSLLFVHDHTGLAKVMMIDFGKTVALLPHQTHSLRLPWAEGNREGDYL 137  
Db 1265 KCHEVIGSSLLFTHDKKEQAKVMMIDFGKTTPLPREGQTLQHDVPWQEGNREGDYL 1319

RESULT 8  
US-11-097-143-1725

; Sequence 1725, Application US/11097143  
; Publication No. US2005020858A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1725  
; LENGTH: 382  
; TYPE: PRT  
; ORGANISM: DROSOPHILA  
US-11-097-143-1725

Query Match 55.7%; Score 403.5; DB 6; Length 382;  
Best Local Similarity 56.9%; Pred. No. 2.2e-36;  
Matches 78; Conservative 19; Mismatches 39; Indels 1; Gaps 1;

Qy 1 AVTKRYMQRMTWSSTLTGFRIGIKADGCTNPFKKTQALEQVTKVLEDFVDDHY 60  
Db 196 AVTKRYMQRMTWSSTLTGFRIGIKSDGTSKDPKTTKSRQIKLAFLELSGPH 255  
Qy 61 ILQKYVACLEALREALEISPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTVALLPHQ 120  
Db 256 ILPRYIORLRAIRATLAVSEFFQTHEVIGSSLLFVHDQTH-ASIMLIDFAKVELLPOLR 314  
Qy 121 LSHRLPWAEGNREGDYL 137  
Db 315 IDHYSANKVGNHEDYL 331

RESULT 9  
US-10-042-894A-25

; Sequence 25, Application US/10042894A  
; Publication No. US2003009011A1  
; GENERAL INFORMATION:  
; APPLICANT: Shi, Jinrui  
; APPLICANT: Beach, Larry  
; APPLICANT: Wang, Hongyu  
; APPLICANT: Rafalski, Antoni J.  
; APPLICANT: Cahoon, Rebecca E.  
; TITLE OF INVENTION: No. US2003009011A1e1 Inositol Polyphosphate Kinase  
; FILE REFERENCE: 1286  
; CURRENT APPLICATION NUMBER: US/10/042,894A  
; CURRENT FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: US 60/261,465  
; PRIOR FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-10-042-894A-25

Query Match 52.8%; Score 382.5; DB 4; Length 316;  
Best Local Similarity 55.1%; Pred. No. 3.9e-34;  
Matches 75; Conservative 19; Mismatches 41; Indels 1; Gaps 1;

Qy 2 VTKPRYMQRMTWSSTLTGFRIGIKADGCTNPFKKTQALEQVTKVLEDFVDDHY 61  
Db 149 VTKPRYMQRMTWSSTLTGFRIGIKSDGTSKDPKTTKSRQIKLAFLELSGPH 208  
Qy 62 LQKYVACLEALREALEISPFKTHEVVGSSLLFVHDHTGLAKVMMIDFGKTVALLPHQ 121  
Db 209 IPKYINRLRAIRATLAVSEFFQTHEVIGSSLLFVHDSKN-ANIMLIDFAKVELLPDIRI 267  
Qy 122 SHRLPWAEGNREGDYL 137  
Db 268 NHTSEVYVGNHEDYL 283



RESULT 10  
US-10-029-386-29832  
/ Sequence 29832, Application US/10029386  
/ Publication No. US20030194704A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Penn, Sharon G.  
/ APPLICANT: Rank, David R.  
/ APPLICANT: Hanzel, David K.  
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C  
/ FILE REFERENCE: AEWICA-X-2  
/ CURRENT APPLICATION NUMBER: US/10/029,386  
/ CURRENT FILING DATE: 2001-12-20  
/ NUMBER OF SEQ ID NOS: 34288  
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
/ SEQ ID NO 29832  
/ LENGTH: 71  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ OTHER INFORMATION: MAP TO CHR19.1  
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.86  
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.69  
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.85  
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.97  
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
/ OTHER INFORMATION: SWISSPROT HIT: P17105, EVALUATION 1.00e-27  
US-10-029-386-29832

Query Match 20.0%; Score 145; DB 4; Length 71;  
Best Local Similarity 100.0%; Pred. No. 2.7e-08;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVTKRYMOWRETMSTSLGFRIGIX 28  
DB 44 AVTKRYMOWRETMSTSLGFRIGIX 71

RESULT 11  
US-10-408-765A-1520  
/ Sequence 1520, Application US/10408765A  
/ Publication No. US20040101874A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ghosh, Soumitra S.  
/ APPLICANT: Fahy, Boi D.  
/ APPLICANT: Zhang, Bing  
/ APPLICANT: Gibson, Bradford W.  
/ APPLICANT: Taylor, Steven W.  
/ APPLICANT: Glenn, Gary M.  
/ APPLICANT: Warnock, Dale E.  
/ TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
/ FILE REFERENCE: 660088,465  
/ CURRENT APPLICATION NUMBER: US/10/408,765A  
/ CURRENT FILING DATE: 2003-04-04  
/ NUMBER OF SEQ ID NOS: 3077  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 1520  
/ LENGTH: 325  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-408-765A-1520

Query Match 11.2%; Score 81.5; DB 4; Length 325;  
Best Local Similarity 32.7%; Pred. No. 2.7;  
Matches 32; Conservative 7; Mismatches 26; Indels 33; Gaps 6;

QY 6 RYMOWR-----ETWST--STLG-----FRIGIKAD-GTCNTNFKTKQALEQVTK 49  
DB 144 RYVMMRWGILMSYTMSTFGSGTIGNKRDTHTIEDLSLGHVCDT----- 190  
QY 50 VLEDFVDDHYILQRYVACLELRALHISPPFKTHEV 87

DB 191 -LLDFCDPDQI---KFTQCLAEIKELRQETIHKKFHEL 224

RESULT 12  
US-10-369-493-175  
/ Sequence 175, Application US/10369493  
/ Publication No. US20030233675A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cao, Yongwei  
/ APPLICANT: Hinkle, Gregory J.  
/ APPLICANT: Slater, Steven C.  
/ APPLICANT: Goldman, Barry S.  
/ APPLICANT: Chen, Xiandeng  
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
/ FILE REFERENCE: 38-10(52052)B  
/ CURRENT APPLICATION NUMBER: US/10/369,493  
/ CURRENT FILING DATE: 2003-02-28  
/ PRIOR APPLICATION NUMBER: US 60/360,039  
/ PRIOR FILING DATE: 2002-02-21  
/ NUMBER OF SEQ ID NOS: 47374  
/ SEQ ID NO 175  
/ LENGTH: 349  
/ TYPE: PRT  
/ ORGANISM: Xenorhabdus nematophilus  
/ FEATURE:  
/ NAME/KEY: unsure  
/ LOCATION: (1)..(349)  
/ OTHER INFORMATION: unsure at all Xaa locations  
US-10-369-493-175

Query Match 11.1%; Score 80.5; DB 4; Length 349;  
Best Local Similarity 24.6%; Pred. No. 3.9;  
Matches 31; Conservative 16; Mismatches 60; Indels 19; Gaps 6;

QY 14 MSSTSLGFRIGIKAD--GTCNTN-----FKTKQALEQVTKVLEDFVDDHYILQRY 65  
DB 191 LSNEDTDFKFDYISRPLOCICINISLPMWELFCNDSDIELISPL-----GKTKQPSY 244  
QY 66 VACLELRALHISPPFKTHEVVGSSLLFVHDHTGLAKVMWIDFKTVALLPDHQTLSHRL 125  
DB 245 AALHLEY-AGEVEVPVFQGNHIASSDIKFIHFGAPMMW-DGFGKAVDADKM---HNI 299  
QY 126 PWASGN 131  
DB 300 GQKTGN 305

RESULT 13  
US-11-096-568A-32990  
/ Sequence 32990, Application US/11096568A  
/ Publication No. US20060048240A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Alexandrov, Nickolai et al.  
/ TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides  
/ FILE REFERENCE: 2750-1592PUS2  
/ CURRENT APPLICATION NUMBER: US/11/096,568A  
/ CURRENT FILING DATE: 2005-04-01  
/ NUMBER OF SEQ ID NOS: 34471  
/ SEQ ID NO 32990  
/ LENGTH: 248  
/ TYPE: PRT  
/ ORGANISM: Arabidopsis thaliana  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ LOCATION: (1)..(248)  
/ OTHER INFORMATION: Ceres Seq. ID no. 13601691  
US-11-096-568A-32990

Query Match 11.0%; Score 79.5; DB 6; Length 248;  
Best Local Similarity 20.5%; Pred. No. 3.2;  
Matches 31; Conservative 31; Mismatches 44; Indels 45; Gaps 5;

[illegible]

Search completed: May 21, 2006, 04:30:06  
Job time : 177 secs



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Publication No. US2006008828A1
GENERAL INFORMATION:
APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
APPLICANT: Vicente E.
TITLE OF INVENTION: Polycystic Kidney Disease Disease Nucleic Acids
FILE REFERENCE: 07039/386US1
CURRENT APPLICATION NUMBER: US/10/501,834
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: PCT/US03/02038
PRIOR FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: 60/351,110
PRIOR FILING DATE: 2002-01-23
NUMBER OF SEQ ID NOS: 221
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 4059
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: VARIANT
LOCATION: 2511
OTHER INFORMATION: Xaa = Pro or Ser
FEATURE:
NAME/KEY: VARIANT
LOCATION: 2981
OTHER INFORMATION: Arg or Gln
US-10-501-834-6

Query Match          9.0%; Score 65; DB 6; Length 4059;
Best Local Similarity 24.1%; Pred. No. 34;
Matches 38; Conservative 21; Mismatches 51; Indels 48; Gaps 8;

Qy      9 QMRRTMSTSTLGRIRISIKKADGTCNTNPK-----KTOALQGYTK----- 49
Db      2459 RWEIITISNTYVNF--DNCVAIRFCSCFGQGGYTKTKQLKRVSSNIVAFXPAA 2516
Qy      50 VLEDF-----VDDGVILQKYVACLEELREALISPPFK--THEVVGSSLLFVHDHTG 100
Db      2517 VLEDDGSLSGKNSHYL-----ASMERTLSPTCLTNASFSQIVGSGVGEAVLTHRMISA 2571

Qy      101 LAKYVMIDFGKTVALPD-----HQTLSHRLPW 127
Db      2572 LAN--SLDVPKRLITTDISNKTITVNYVEDTLSNYGW 2607

RESULT 3
US-10-510-162-4
Sequence 4, Application US/10510162
Publication No. US20060099580A1
GENERAL INFORMATION:
APPLICANT: Corena T. McMANUS
APPLICANT: David A. JONES
TITLE OF INVENTION: METHYL-CPG BINDING DOMAIN PROTEIN 2 HOMOLOGS
FILE REFERENCE: 38509-0016US1
CURRENT APPLICATION NUMBER: US/10/510,162
CURRENT FILING DATE: 2004-10-05
PRIOR APPLICATION NUMBER: PCT/US03/10631
PRIOR FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 60/369,851
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 194
TYPE: PRT
ORGANISM: Homo sapiens
US-10-510-162-4

Query Match          8.8%; Score 64; DB 6; Length 194;
Best Local Similarity 25.3%; Pred. No. 0.71;
Matches 25; Conservative 20; Mismatches 36; Indels 18; Gaps 6;
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```
Qy      6 RYMQWRETMSSTSLGF--RIEGRK--KADGTCNTNFKTQALBQVT-----KVLEDFV 55
Db      51 RYHQMEEELKPPQVQWGRLOGLQAVSAGSELSTLDLANTLQKLVPSYTGSLLEDLA 110

Qy      56 DG-DHYVLQKYVACLEELREALISPPFKTHEVVGSSLL 93
Db      111 SGLEHSCPMPLACSS---DAVEIIP---AEVGISQL 142

RESULT 4
US-10-525-621-1
Sequence 1, Application US/10525621
Publication No. US20060100418A1
GENERAL INFORMATION:
APPLICANT: Kiyosue, Yuko
APPLICANT: Sasaki, Hiroyuki
APPLICANT: Teukita, Shoichiro
APPLICANT: Eisai Co., Ltd.
TITLE OF INVENTION: CULTURED XENOPUS LAEVIS CELL LINES
FILE REFERENCE: 082368-002400US
CURRENT APPLICATION NUMBER: US/10/525,621
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: PCT/JP03/10434
PRIOR FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: JP 2002-241487
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2829
TYPE: PRT
ORGANISM: Xenopus laevis
US-10-525-621-1

Query Match          8.6%; Score 62; DB 6; Length 2829;
Best Local Similarity 24.2%; Pred. No. 48;
Matches 24; Conservative 16; Mismatches 43; Indels 16; Gaps 2;

Qy      5 PRYMQWRETMSSTSLGFRIEGRKAD-----GTCNTNFKKTQALBQVT 49
Db      2553 PRYSTWRTSSSSILASSESSSEKASEDEKQOVCSPPGPRSECSSAGTKWIKISE 2612

Qy      50 VLEDFVDDHYVLQKYVACLEELREALISPPFKTHEV 87
Db      2613 ILFTPSNGSSSTIAESNCSELSKTLVYQMAPAVSKTBDV 2651

RESULT 5
US-10-706-435A-26
Sequence 26, Application US/10706435A
Publication No. US20060088547A1
GENERAL INFORMATION:
APPLICANT: Walter Reed Army Institute of Research
APPLICANT: Ianar, David E.
APPLICANT: Hillier, Collette J.
APPLICANT: Lyon, Jeffrey A.
APPLICANT: Angov, Evelina
APPLICANT: Kumar, Sanjay
APPLICANT: Rogers, William
APPLICANT: Barbosa, Arnoldo
TITLE OF INVENTION: Expression, Purification, and Uses of a Plasmodium
FILE REFERENCE: 003/285/SAP
CURRENT APPLICATION NUMBER: US/10/706,435A
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/425,719
PRIOR FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Word XP
SEQ ID NO 26
LENGTH: 456
TYPE: PRT
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ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: LSA-NRC (H) protein  
US-10-706-435A-26

Query Match 8.5%; Score 61.5; DB 6; Length 456;  
Best Local Similarity 29.5%; Pred. No. 4.6;  
Matches 28; Conservative 15; Mismatches 25; Indels 27; Gaps 5;

Qy 23 RIEGKKKADGTCNTNF-----KKTQALBQVTKVLEDFV-----DGDHVLQ 63  
Db 369 KIKKKKTEKTKNDNFKNRDSLYDHNKTKYNDQVNEKSKFTKSLFHFIDGNEILQ 428

Qy 64 KYVACLEELREALBISPFKTHEVVSSLLFVYDH 98  
Db 429 ----IVDELSE--DITKTFM--KLGGSGSPHHHH 455

## RESULT 6

US-10-196-749-574  
Sequence 574, Application US/10196749  
Publication No. US20060094864A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jlan  
APPLICANT: Deenoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACTIS ENCODING THE SAME

CURRENT FILING DATE: 2002-07-16  
PRIORITY FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 10/052586  
PRIORITY FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 60/059263  
PRIORITY FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059266  
PRIORITY FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/062250  
PRIORITY FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063120  
PRIORITY FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063121  
PRIORITY FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063486  
PRIORITY FILING DATE: 1997-10-21

PRIOR APPLICATION NUMBER: 60/063540  
PRIORITY FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063541  
PRIORITY FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063544  
PRIORITY FILING DATE: 1997-10-28

PRIOR APPLICATION data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612

SEQ ID NO 574  
LENGTH: 882

TYPE: PRT  
ORGANISM: Homo Sapien

US-10-196-749-574

Query Match 8.4%; Score 61; DB 6; Length 882;  
Best Local Similarity 25.6%; Pred. No. 13;  
Matches 21; Conservative 14; Mismatches 41; Indels 6; Gaps 3;

Qy 28 KKADGTCNTNFKTKQALBQVTKVLEDFVYDGHV--IIQKTV--VACLEELREALBISPF 82

Db 355 RKDGLCPDPFRKQVBPASNYLDQMEYDYKVEEISRKHKNGFCIOGVSSGLR-QPVG 413  
Qy 83 KTHFVGSLLFVYDHTGLAKY 104  
Db 414 ALHSGDGSQRLFILEKEGYVKI 435

## RESULT 7

US-10-370-959-11

Sequence 11, Application US/10370959  
Publication No. US20060088907A1  
GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc  
APPLICANT: Meyers, Rachel E.  
APPLICANT: Williamson, Mark W.  
APPLICANT: Kapeller-Libermann, Rosana  
APPLICANT: Macbeth, Kyle J.  
APPLICANT: Hunter, John J.  
APPLICANT: Bandaru, Rajasekhar  
APPLICANT: Tsai, Fong-Ying

TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,  
TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,  
TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863 AND  
TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR

FILE REFERENCE: MPI03-0170NMIM  
CURRENT APPLICATION NUMBER: US/10/370, 959  
CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: US 09/910,150  
PRIORITY FILING DATE: 2001-07-18

PRIOR APPLICATION NUMBER: US 60/219,028  
PRIORITY FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: US 10/251,507  
PRIORITY FILING DATE: 2002-09-20

PRIOR APPLICATION NUMBER: US 09/715,479  
PRIORITY FILING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: US 60/218,053  
PRIORITY FILING DATE: 2000-07-13

PRIOR APPLICATION NUMBER: US 09/644,929  
PRIORITY FILING DATE: 2000-08-23

PRIOR APPLICATION NUMBER: US 60/212,439  
PRIORITY FILING DATE: 2000-06-16

PRIOR APPLICATION NUMBER: US 09/892,870  
PRIORITY FILING DATE: 2001-06-26

PRIOR APPLICATION NUMBER: US 60/214,174  
PRIORITY FILING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: US 09/775,117  
PRIORITY FILING DATE: 2001-02-01

Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 156

SOFTWARE: PASCSEQ for Windows Version 4.0  
SEQ ID NO 11

LENGTH: 926  
TYPE: PRT

ORGANISM: Homo Sapiens  
US-10-370-959-11

Query Match 8.3%; Score 60; DB 6; Length 926;  
Best Local Similarity 26.0%; Pred. No. 18;  
Matches 26; Conservative 16; Mismatches 42; Indels 16; Gaps 3;

Qy 43 ALBQVTKVLEDFVQ-----DHYIIQKYVACLEELREALBISPFKTHEVVGSLL 93  
Db 590 ALBICRASLOEYVENPDLRGISPEYVLDQMSGLAHLSLHIVHDLKP-----GNILL 645

Qy 94 FVYDHTGLAKYMMIDRGKTVALLPDHQ---TLSHRLPWAEG 130  
Db 646 TGPDSQGLGRVVALSDPGLCKKLPAGRCFSLSHGIGTTEG 685

## RESULT 8

US-11-246-999-49  
Sequence 49, Application US/11246999

Publication No. US2006009622A1  
GENERAL INFORMATION:  
APPLICANT: N1 et al.  
TITLE OF INVENTION: 12 Human Secreted Proteins  
FILE REFERENCE: FP469P2  
CURRENT APPLICATION NUMBER: US/11/246,999  
PRIOR FILING DATE: 2005-10-11  
PRIOR APPLICATION NUMBER: US/09/984,130  
PRIOR FILING DATE: 2001-10-29  
PRIOR APPLICATION NUMBER: 60/243,792  
PRIOR FILING DATE: 2000-10-30  
PRIOR APPLICATION NUMBER: 09/836,353  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: 60/198,407  
PRIOR FILING DATE: 2000-04-19  
PRIOR APPLICATION NUMBER: PCT/US99/25031  
PRIOR FILING DATE: 1999-10-27  
PRIOR APPLICATION NUMBER: 60/105,971  
PRIOR FILING DATE: 1998-10-28  
NUMBER OF SEQ ID NOS: 149  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 49  
LENGTH: 700  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-246-999-49

Query Match 8.1%; Score 59; DB 7; Length 700;  
Best Local Similarity 25.6%; Pred. No. 17;  
Matches 21; Conservative 13; Mismatches 42; Indels 6; Gaps 3;

QY 28 KKADGTGNTNFKTQALAEQVTVLEDFVGDH--IIQK---VACIELEALEISPPF 82  
DB 173 RKDGLCFPPDPRRQVGPASNYLGQMEDYKVGISRKHKMCLCQEVWSGLR-QPVS 231  
QY 83 KTHEVVGSSLLFVHDHTGLAV 104  
DB 232 AVHSGDGSRLFILEKEGYVKI 253

RESULT 9  
US-11-146-700-1  
Sequence 1, Application US/11/146700  
Publication No. US20060094100A1  
GENERAL INFORMATION:  
APPLICANT: Columbia University  
APPLICANT: Tong, Liang  
APPLICANT: Jogi, Gerwald  
TITLE OF INVENTION: STRUCTURAL MODELS OF CARINITINE  
FILE REFERENCE: 070050.2801  
CURRENT APPLICATION NUMBER: US/11/146,700  
CURRENT FILING DATE: 2005-06-07  
PRIOR APPLICATION NUMBER: PCT/US04/00170  
PRIOR FILING DATE: 2004-01-06  
PRIOR APPLICATION NUMBER: 60/438,172  
PRIOR FILING DATE: 2003-01-06  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 626  
TYPE: PRT  
ORGANISM: Mus musculus  
US-11-146-700-1

Query Match 8.1%; Score 58.5; DB 7; Length 626;  
Best Local Similarity 21.6%; Pred. No. 16;  
Matches 40; Conservative 21; Mismatches 55; Indels 69; Gaps 10;

QY 4 KRYWQWRETMSTSTLGF-----RIEIGIKKADGTGNTNFKKTQAL 44  
DB 104 KTRVLOFPQPVVYISSPVLTPKQDVEDVLOGQLRFAKLIIEGV-----LDFK--SMI 153

QY 45 EQVTVLEDFVGDHVILOKQVACIELEALEISPPF-----FPK-----THEVVGSSL 92  
DB 154 DNETLPEV-FLGGQPLCMQYQIILSSCR---EVEPKQDSVNFILSKSRPFHITVYHY 209  
QY 93 LP-----VHDHTS-----LAKVMIDFGKTVLPDHTLSRLPMAEG----- 130  
DB 210 QFFELDVYHNDGTPLTSDQIFVQLEKIWNLSIQSNKEPVGILTSNHRMTAKAYNNLIKD 269  
QY 131 --NRE 133  
DB 270 KVNRE 274

RESULT 10  
US-10-511-937-2968  
Sequence 2968, Application US/10511937  
Publication No. US2006008836A1  
GENERAL INFORMATION:  
APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
APPLICANT: Wohlgemuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
APPLICANT: Prentice, James  
APPLICANT: Morris, Macdonald  
APPLICANT: Rosenberg, Steven  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
FILE REFERENCE: 50661200104  
CURRENT APPLICATION NUMBER: US/10/511,937  
CURRENT FILING DATE: 2004-10-19  
PRIOR APPLICATION NUMBER: PCT/US2003/012946  
PRIOR FILING DATE: 2003-04-24  
PRIOR APPLICATION NUMBER: US 10/131,831  
PRIOR FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: US 10/325,899  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 3117  
SOFTWARE: Patent In version 3.2  
SEQ ID NO 2968  
LENGTH: 1866  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-511-937-2968

Query Match 8.1%; Score 58.5; DB 6; Length 1866;  
Best Local Similarity 20.3%; Pred. No. 73;  
Matches 30; Conservative 20; Mismatches 39; Indels 59; Gaps 6;

QY 26 GIKKADGTGNTNFKTQALAEQVTVLEDFVD-----GDHVILOKQV 67  
DB 119 GLKRPPOSCSSPPRCKQQLAKKYLOLRTSAQRYRSQIPSGQPHAFHYVP 178  
QY 68 CLEELREA-----LEISPFKTHEVVGSSLLFVHDHTGLAKW 105  
DB 179 PI--LRRTATSLDTPREGALMGDVKEADVISDLDFTVRNKGPRVTVLIGKAGM----- 232  
QY 106 MIDFGKTVLPDHTLSRL--PWAEGN 131  
DB 233 ----GKT-----TLAHLCOKWAEGH 249

RESULT 11  
US-11-264-784-63  
Sequence 63, Application US/11264784  
Publication No. US20060094092A1  
GENERAL INFORMATION:  
APPLICANT: E.I. duPont de Nemours & Co., Inc.  
APPLICANT: Damude, Howard Glenn  
APPLICANT: Gillies, Peter John  
APPLICANT: Macool, Daniel Joseph  
APPLICANT: Picataggio, Stephen K.  
APPLICANT: Pollak, Dana M. Walters

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; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 63
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Candida albicans (GenBank Accession No. EAL04510)
US-11-264-784-63

Query Match
Best Local Similarity 23.9%; Score 58; DB 7; Length 353;
Matches 21; Conservative 16; Mismatches 21; Indels 30; Gaps 7;

Qy 50 VLEDFVDDGHVTLQKY--VACLELRREALISPPFK-----THEVVGSSLLFVNDHT 99
Db 245 VFNSFT---HSLMIFYFSLSCLK-----IRVPNFKRIITMQITQFTVGSIALIHSP- 295
Qy 100 GLAKVMIDFKQVVALPDHQTLSHRLPW 127
Db 296 ----VMIVDTSHVIS-PDN-----LKN 312

RESULT 12
US-10-505-928-519
; Sequence 519, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO: 519
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-519

Query Match
Best Local Similarity 7.9%; Score 57.5; DB 6; Length 192;
Matches 26; Conservative 23; Mismatches 45; Indels 9; Gaps 4;

Qy 8 MOWETMSSTSLGFRIGIKKADGTC---NTNFKTQALBQVTKVLEDF---VDG-DHV 60
Db 33 LKFNIEFVTVPTIGTNEKIKLSNGTAKGISCHFWDGQEKLRPMKYSRCIDGITIV 92
Qy 61 ILQKTVACLELRREALISPPFKTHEVVGSSLLFVNDHTGLAK 103
Db 93 VDSVDVRLERAK--TELRKTKFAENGSTPLVLVANKQDLPRK 133

RESULT 13
US-10-505-928-209
; Sequence 209, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
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; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO: 209
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-209

Query Match
Best Local Similarity 7.7%; Score 56; DB 6; Length 288;
Matches 31; Conservative 15; Mismatches 43; Indels 38; Gaps 8;

Qy 10 WRETMSSTSLGFRIGIKKADGTCNTNFKTQALBQVTKVLEDFVDGHVTLQKYVAC 68
Db 16 WEECFQAAVQALRAGQIIRKALTEKKVSTKTSAAADLVET-----DHLVEDLIIS- 67
Qy 69 LEELREALISPPFKTHEVVGSSLLFVNDHTGLAKVMIDFKQVVALPDHQTLSH 121
Db 68 --ELRR-----PESHFRFIEAASGAKCVLTHSPT---WITD-----PIDGTC 107
Qy 122 S--HRLP 126
Db 108 NFVHRFP 114

RESULT 14
US-10-706-435A-4
; Sequence 4, Application US/10706435A
; Publication No. US20060088547A1
; GENERAL INFORMATION:
; APPLICANT: Walter Reed Army Institute of Research
; APPLICANT: Lanar, David B.
; APPLICANT: Hillier, Collette J.
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Angov, Evelina
; APPLICANT: Kumar, Sanjai
; APPLICANT: Rogers, William
; APPLICANT: Barbosa, Arnoldo
; TITLE OF INVENTION: Expression, Purification, and Uses of a Plasmidum
; FILE REFERENCE: 003/285/SAP
; CURRENT APPLICATION NUMBER: US/10/706,435A
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,719
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word XP
; SEQ ID NO: 4
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: LSA-NRC(H)Mut
US-10-706-435A-4

Query Match
Best Local Similarity 7.7%; Score 56; DB 6; Length 457;
Matches 26; Conservative 16; Mismatches 27; Indels 26; Gaps 4;

Qy 23 RIBGIRKADGTCNTNFK-----KKTQALBQVTKVLEDFV-----DGDHVTILO 63
Db 369 KIKGKKYKTKYKNNFPPNDKSLYDEHIKKYKNDQVNEKKEKFKSLFHFIPGDNEILO 428
Qy 64 KYVACLELRREALISPPFKTHEVVGSSLLFVNDH 98
Db 429 ----LYDELSIEDITKTFM--KLGGSGSPHHNNH 456

RESULT 15
US-10-511-937-2929
; Sequence 2929, Application US/10511937
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